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Der Präsident des Europäischen Patentamts;
Im Auftrag

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Identification of novel E2F target genes and use thereof

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047-E2F-PROV

IDENTIFICATION OF NOVEL E2F TARGET GENES AND USE THEREOF

The present invention concerns modifying plant characteristics. More particularly, the present invention relates to identification of genes and proteins involved in E2Fa/Dpa-mediated processes and further relates to use of such genes and proteins for modifying characteristics in plants.

Growth, development and differentiation of higher organisms are controlled by a highly ordered set of events called the cell cycle (Morgan, 1997). Cell division and cell growth are operated by the cell cycle, which ensures correct timing and high fidelity of the different transition events involved. Cell cycle regulation at both G1→S and G2→M phase transitions depends on the formation of appropriate protein complexes and both transitions are believed to be the major control points in the cell cycle. The cell's decision to proliferate and synthesize DNA and ultimately to divide is made at the G1→S restriction point in late G1. Overcoming this point of no return requires the cell's competence to initiate DNA synthesis as well as the expression of S-phase genes. Transcription of S-phase-specific genes requires binding to the DNA of an E2F transcription factor. Dimerisation of E2F with DP is a prerequisite for high affinity binding to the E2F consensus DNA binding site (TTT(C/G)(C/G)CGC), that can be found in the promoters of genes involved in DNA replication, repair, checkpoint control and differentiation (Ren et al., 2002; Weinmann et al., 2001; Kel et al., 2001). Variants of this consensus sequence as well as other locations of this consensus sequences are also found..The heterodimeric E2F/dimerization partner (DP) transcription factor also regulates the promoter activity of multiple genes, which are essential for DNA replication and cell cycle control (Helin, 1998; Müller and Helin, 2000). E2F transcription factors are critical effectors of the decision to pass the restriction point and to allow the cell to proceed in S-phase.

In the Arabidopsis genome, 3 E2F (E2Fa, E2Fb, and E2Fc) and 2 DP genes (DPa and DPb) are present (Vandepoele et al., 2002). The phenotypic analysis of plants overexpressing the E2Fa/DPa geneswas described recently (De Veylder et al., 2002). Microscopic analysis revealed that E2Fa/DPa overproducing cells underwent ectopic cell division or endoreduplication, depending on the cell type. Whereas extra cell divisions resulted in cells being smaller than those seen in the same tissues of control plants, extra endoreduplication caused formation of giant nuclei. By RT-PCR it was demonstrated that expression levels of genes involved in DNA replication (CDC6, ORC1, MCM, DNA pol α) were strongly upregulated in plants overexpressing E2Fa and Dpa (De Veylder et al., 2002).

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The aim of the present invention is to identify genes having altered expression levels in plants overexpressing E2Fa and Dpa relative to expression levels in corresponding wild type plants. Furthermore, it is the aim of the present invention to provide means to modulate expression of these genes, which in turn allows for modulation of the biological processes that they control. It is the aim of the present invention to mimic E2F/DP activity by manipulating downstream factors involved in E2F/DP pathways. This strategy allows a fine-tuning of the effects of E2Fa/DPa,. Whereas overexpression of E2Fa or DP or both can be pleiotropic, it is the aim of the invention to provide methods to alter plant characteristics in a more controlled and targeted way. Modulation of particular biological processes can give rise to plants having altered characteristics, which can have particularly useful applications in agriculture and horticulture.

The present invention concerns a method for modifying plant characteristics, such as plant growth, plant yield, development, biochemistry, physiology, architecture or stress tolerance by modulation of the genes according to the present invention and/or by modulation of the proteins encoded by these genes. The present invention also concerns genetic constructs for performing the methods of the invention and to plants or plant parts obtainable by the methods of the present invention, which plants have altered characteristics compared to their otherwise isogenic counterparts. The invention also extends to recombinant nucleic acids and the use thereof in the methods according to the invention.

The inventors designed a microarray experiment, comparing transcript levels of more than 4579 genes of wild type and transgenic Arabidopsis lines overexpressing E2Fa/DPa. Surprisingly, the inventors found that a wide variety of classes of genes are up or down regulated in E2Fa-Dpa overexpressing plants. These sequences are represented with their (Munich information center for protein sequences (MIPS) accession number in tables 4 and 5. Further classification of these genes according to their function is provided in Tables 1 and 2. Sequences which were at least 2-fold upregulated or 2-fold downregulated are shown in Tables 1 and 2, respectively. Promoter analysis of these genes allowed for the identification of genes under the direct control of E2Fa and/or DPa proteins and genes that are indirectly controlled by the E2Fa/DPa complex. Examples of mechanisms for such indirect control include, (i) recognition by E2F/DP of other sequence elements that diverge from the consensus recognition site; (ii) possible association of E2F/DP with other DNA binding proteins capable of recognizing other DNA elements; and (iii) sequential transcription activation of a first gene capable of regulating transcription of a second gene. It is to be understood that having an E2F target sequence is not a prerequisite to be regulated by E2F.

The gene that corresponds to the sequence deposited under the database accession number At1g57680 (accession number of the MIPS MATDB database, http://mips.gsf.de/proj/thal/db/index.html) is an example of a gene which is likely to be under the indirect control of the E2Fa/Dpa complex. This gene is of unknown function. It was surprising to find this unknown gene and the other genes of Tables 1, 2, 4 and 5 to be involved in E2Fa/Dpa controlled processes.

Therefore, according to the present invention, there is provided a method to alter plant characteristics, comprising modifying expression of one or more nucleic acids and/or modifying the activity of one or more proteins, which nucleic acids or proteins are essentially similar to any one of SEQ ID NO 1 to 104 and/or to a nucleic acid sequence or protein sequence deposited under accession number At1g57680 and/or deposited under any of the accession numbers presented in Tables 1, 2, 4 and 5.

The term "modifying the expression" relates to increasing or decreasing or altering in time or place the expression of a nucleic acid. According to the invention, the "nucleic acid" or the "gene" may be the wild type, i.e. native or endogenous or heterologous, i.e. derived from another individual plant or plant species. The gene (transgene) may be substantially modified from its native form in composition and/or genomic environment through deliberate human manipulation. This transgene can be introduced into a host cell by transformation techniques. Also expression of the native genes can be modified by introduction in the plant of regulatory sequences capable of altering expression of the native gene. The term "modifying the activity" relates to enhancing, or decreasing or altering in time or place the activity of a protein or polypeptide. According to the invention, the "protein" or the "polypeptide" may be the wild type protein, i.e. native or endogenous, or alternatively, the protein may be heterologous, i.e. derived from another individual or species.

The term "essentially similar to" a protein or a gene of the present invention as used herein includes homologues, derivatives and functional fragment thereof. The term "essentially similar to" also includes at least a part of the protein or gene in question; a complement of the protein or gene; RNA, DNA, a cDNA or a genomic DNA corresponding to the protein or gene; a variant of the gene or protein due to the degeneracy of the genetic code; a family member of the gene or protein; an allelic variant of the gene or protein; and different splice variant of the gene or protein and variants that are interrupted by one or more intervening sequences. Advantageously, nucleic acids or proteins essentially similar to the proteins and nucleic acids according to the invention may be used in the methods of the present invention.

"Homologues" of the proteins of the present invention encompass peptides, oligopeptides, polypeptides, proteins and enzymes having amino acid substitutions, deletions and/or additions relative to the protein in question and having similar biological and functional activity as an unmodified protein from which they are derived. To produce such homologues, amino acids of the protein may be replaced by other amino acids having similar properties (such as similar hydrophobicity, hydrophilicity, antigenicity, propensity to form or break α-helical structures or β-sheet structures). Conservative substitution tables are well known in the art (see for example Creighton (1984) Proteins. W.H. Freeman and Company). The homologues useful in the method according to the invention may have at least 50% sequence identity or similarity (functional identity) to the unmodified protein, alternatively at least 60% sequence identity or similarity to an unmodified protein, or alternatively at least 70% sequence identity or similarity to an unmodified protein. Typically, the homologues have at least 80% sequence identity or similarity to an unmodified protein, preferably at least 85% sequence identity or similarity, further preferably at least 90% sequence identity or similarity to an unmodified protein, most preferably at least 95% sequence identity or similarity to an unmodified protein. This % identity can be calculated using the Gap program in the WISCONSIN PACKAGE version 10.0-UNIX from Genetics Computer Group, Inc based on the method of Needleman and Wunsch (J. Mol. Biol. 48:443-453 (1970)) using the set of default parameters for pairwise comparison (for amino acid sequence comparison: Gap Creation Penalty = 8, Gap Extension Penalty = 2; for nucleotide sequence comparison: Gap Creation Penalty = 50; Gap Extension Penalty = 3)

Methods for the search and identification of other homologues of the proteins of the present invention, or for nucleic acid sequences encoding homologues of proteins of the present invention would be well known to person skilled in the art. Methods for the alignment of sequences for comparison are well known in the art, such methods include GAP, BESTFIT, BLAST, FASTA and TFASTA. The BLAST algorithm calculates percent sequence identity and performs a statistical analysis of the similarity between the two sequences. The software for performing BLAST analysis is publicly available through the National Center for Biotechnology Information.

Two special forms of homology, orthologous and paralogous, are evolutionary concepts used to describe ancestral relationships of genes. The term "paralogous" relates to gene-duplications within the genome of a species leading to paralogous genes. The term "orthologous" relates to homologous genes in different organisms due to ancestral relationship.

The term "homologues" as used herein also encompasses paralogues and orthologues of the proteins used in the methods according to the invention.

"Substitutional variants" of a protein are those in which at least one residue in an amino acid sequence has been removed and a different residue inserted in its place. Amino acid substitutions are typically of single residues, but may be clustered depending upon functional constraints placed upon the polypeptide; insertions will usually be of the order of about 1-10 amino acid residues, and deletions will range from about 1-20 residues.

"Insertional variants" of a protein are those in which one or more amino acid residues are introduced into a predetermined site in the protein. Insertions can comprise amino-terminal and/or carboxy-terminal fusions as well as intra-sequence insertions of single or multiple amino acids. Generally, insertions within the amino acid sequence will be smaller than amino- or carboxy-terminal fusions, of the order of about 1 to 10 residues. Examples of amino- or carboxy-terminal fusion proteins or peptides include the binding domain or activation domain of a transcriptional activator as used in the yeast two-hybrid system, phage coat proteins, $(histidine)_6$-tag, glutathione S-transferase-tag, protein A, maltose-binding protein, dihydrofolate reductase, Tag•100 epitope, c-myc epitope, FLAG®-epitope, lacZ, CMP (calmodulin-binding peptide), HA epitope, protein C epitope and VSV epitope.

"Deletion variants" of a protein are characterized by the removal of one or more amino acids from the protein. Amino acid variants of a protein may readily be made using peptide synthetic techniques well known in the art, such as solid phase peptide synthesis and the like, or by recombinant DNA manipulations. The manipulation of DNA sequences to produce substitution, insertion or deletion variants of a protein are well known in the art. For example, techniques for making substitution mutations at predetermined sites in DNA are well known to those skilled in the art and include M13 mutagenesis, T7-Gen *in vitro* mutagenesis (USB, Cleveland, OH), QuickChange Site Directed mutagenesis (Stratagene, San Diego, CA), PCR-mediated site-directed mutagenesis or other site-directed mutagenesis protocols.

The term "derivatives" of a protein according to the present invention are those peptides, oligopeptides, polypeptides, proteins and enzymes which may comprise substitutions, or deletions or additions of naturally and non-naturally occurring amino acid residues compared to the amino acid sequence of a naturally-occurring form of the protein as deposited under the accession numbers presented in table 1, 2, 4 and 5. "Derivatives" of a protein of the present invention encompass peptides, oligopeptides, polypeptides, proteins and enzymes which may

comprise naturally occurring altered, glycosylated, acylated or non-naturally occurring amino acid residues compared to the amino acid sequence of a naturally-occurring form of the polypeptide. A derivative may also comprise one or more non-amino acid substituents compared to the amino acid sequence from which it is derived, for example a reporter molecule or other ligand, covalently or non-covalently bound to the amino acid sequence such as, for example, a reporter molecule which is bound to facilitate its detection, and non-naturally occurring amino acid residues relative to the amino acid sequence of a naturally-occurring protein of the present invention.

The expression "functional fragment" of a protein or a nucleic acid refers to a fragment that has at least some contiguous amino acid residues of said protein or at least some contiguous nucleic acid residues, and that has retained the biological activity of said naturally-occurring protein or said nucleic acid.

Advantageously, the method according to the present invention may also be practiced using fragments of DNA or of a nucleic acid sequence. The term "DNA fragment or DNA segment" refers to a piece of DNA derived or prepared from an original (larger) DNA molecule. The term is not restrictive to the content of the DNA fragment or segment, which can be any DNA, with any functionality. For example, the DNA fragment or segments can comprise many genes, with or without additional control elements or may contain just spacer sequences etc.

The present invention also encompasses nucleic acid sequences capable of hybridising with a nucleic acid sequence of the present invention or a nucleic acid encoding a protein according to the present invention. The term "hybridisation" as defined herein is the process wherein substantially homologous complementary nucleotide sequences anneal to each other. The hybridisation process can occur entirely in solution, i.e. both complementary nucleic acids are in solution. Tools in molecular biology relying on such a process include the polymerase chain reaction (PCR; and all methods based thereon), subtractive hybridisation, random primer extension, nuclease S1 mapping, primer extension, reverse transcription, cDNA synthesis, differential display of RNAs, and DNA sequence determination. The hybridisation process can also occur with one of the complementary nucleic acids immobilised to a matrix such as magnetic beads, Sepharose beads or any other resin. Tools in molecular biology relying on such a process include the isolation of poly (A+) mRNA. The hybridisation process can furthermore occur with one of the complementary nucleic acids immobilised to a solid support such as a nitro-cellulose or nylon membrane or immobilised by e.g. photolithography to e.g. a siliceous glass support (the latter known as nucleic acid arrays or microarrays or as nucleic

acid chips). Tools in molecular biology relying on such a process include RNA and DNA gel blot analysis, colony hybridisation, plaque hybridisation, *in situ* hybridisation and microarray hybridisation. In order to allow hybridisation to occur, the nucleic acid molecules are generally thermally or chemically denatured to melt a double strand into two single strands and/or to remove hairpins or other secondary structures from single stranded nucleic acids. The stringency of hybridisation is influenced by conditions such as temperature, salt concentration and hybridisation buffer composition. High stringency conditions for hybridisation include high temperature and/or low salt concentration (salts include NaCl and Na_3-citrate) and/or the inclusion of formamide in the hybridisation buffer and/or lowering the concentration of compounds such as SDS (detergent) in the hybridisation buffer and/or exclusion of compounds such as dextran sulphate or polyethylene glycol (promoting molecular crowding) from the hybridisation buffer. Conventional hybridisation conditions are described in, for example, Sambrook (2001) Molecular Cloning: a laboratory manual, 3rd Edition Cold Spring Harbor Laboratory Press, CSH, New York, but the skilled craftsman will appreciate that numerous different hybridisation conditions can be designed in function of the known or the expected homology and/or length of the nucleic acid sequence. With specifically hybridising is meant hybridising under stringent conditions. Specific conditions for "specifically hybridising" are for example: hybridising under stringent conditions such as a temperature of 60°C followed by washes in 2XSSC, 0.1XSDS, and 1X SSC, 0.1X SDS. Sufficiently low stringency hybridisation conditions are particularly preferred to isolate nucleic acids heterologous to the DNA sequences of the invention defined supra. Elements contributing to heterology include allelism, degeneration of the genetic code and differences in preferred codon usage.

Another method for altering growth characteristics resides in use of a nucleic acid sequence which is an alternative splice variant of a gene of the present invention (deposited in the MIPS database under the accession numbers as presented in Tables 1, 2, 4 or 5). The term "alternative splice variant" as used herein encompasses variants in which introns and selected exons have been excised (for example, such that the mRNA has seed-preferred expression), optionally in response to specific signals. Such variants will be ones in which the biological activity of the proteins of the present invention remains unaffected, which can be achieved by selectively retaining functional segments of the proteins. Methods for making such splice variants are well known in the art.

The term "plant characteristic" means any characteristic of the plant and is also used in the meaning of "growth characteristics". These terms refer to a change in one or more cellular

processes involved in growth and development. These processes encompass, but are not limited to, cell cycle progression, cell division and plant developmental processes, such as pattern formation, differentiation, cell fate etc. A change in one or more of these cellular processes may be manifested by a change in characteristics, such as yield, biomass production, growth rate, plant architecture, number of organs, size of organs, early vigour, survival rate, stress tolerance, senescence, time of flowering, time to flower and more. These characteristics are also encompassed by the term "growth characteristics". The term plant characteristic or growth characteristic further encompasses a change in metabolism, biochemistry and physiology of a plant and more.

"Growth" refers to the capacity of the plant or of plant parts to grow and increase in biomass while "yield" refers to the harvestable biomass of plants or plant parts, particularly those parts of commercial value. Field-grown plants almost always will experience some form of stress, albeit mild, and therefore the terms growth, or yield or biomass production or biomass, do not to distinguish the performance of the plants under non-stressed or under stress conditions. As certain beneficial effects of the invention on growth and yield are expected to occur under both severe and mild stress conditions, they are thus described as increasing growth and/or yield under stressed and non-stressed conditions.

"Plant development" means any cellular process of a plant that is involved in determining the developmental fate of a plant cell, in particular the specific tissue or organ type into which a progenitor cell will develop. Cellular processes relevant to plant development will be known to those skilled in the art. Such processes include, for example, morphogenesis, photomorphogenesis, shoot development, root development, vegetative development, reproductive development, stem elongation, flowering, and regulatory mechanisms involved in determining cell fate, in particular a process or regulatory process involving the cell cycle.

"Plant architecture", as used herein refers to the external appearance of a plant, including any one or more structural features or a combination of structural features thereof. Such structural features include the shape, size, number, position, colour, texture, arrangement, and patternation of any cell, tissue or organ or groups of cells, tissues or organs of a plant, including the root, stem, leaf, shoot, petiole, trichome, flower, petal, stigma, style, stamen, pollen, ovule, seed, embryo, endosperm, seed coat, aleurone, fibre, fruit, cambium, wood, heartwood, parenchyma, aerenchyma, sieve element, phloem or vascular tissue, amongst others.

"Plant biochemistry" is to be understood by those skilled in the art to refer to the metabolic. "Metatbolism" as used in the present ivention is interchangeable with biochemistry. Meatbolism and/or biochemistry encompass catalytic or assimilation or other metabolic processes of a plant, including primary and secondary metabolism and the products thereof, including any element, small molecules, macromolecules or chemical compounds, such as but not limited to starches, sugars, proteins, peptides, enzymes, hormones, growth factors, nucleic acid molecules, celluloses, hemicelluloses, calloses, lectins, fibres, pigments such as anthocyanins, vitamins, minerals, micronutrients, or macronutrients, that are produced by plants.

"Plant physiology" encompasses the functional processes of a plant, including developmental processes such as growth, expansion and differentiation, sexual development, sexual reproduction, seed set, seed development, grain filling, asexual reproduction, cell division, dormancy, germination, light adaptation, photosynthesis, leaf expansion, fiber production, secondary growth or wood production, amongst others; responses of a plant to externally-applied factors such as metals, chemicals, hormones, growth factors, environment and environmental stress factors (e.g. anoxia, hypoxia, high temperature, low temperature, dehydration, light, day length, flooding, salt, heavy metals, amongst others), including adaptive responses of plants to said externally-applied factors.

The term "stress tolerance" is understood as the capability of better survival and/or better performing in stress conditions such as environmental stress, which can be biotic or abiotic. Salinity, drought, heat, chilling and freezing are all described as examples of conditions which induce osmotic stress. The term "environmental stress" as used in the present invention refers to any adverse effect on metabolism, growth or viability of the cell, tissue, seed, organ or whole plant which is produced by a non-living or non-biological environmental stressor. More particularly, it also encompasses environmental factors such as water stress (flooding, water logging, drought, dehydration), anaerobic (low level of oxygen, CO2 etc.), aerobic stress, osmotic stress, salt stress, temperature stress (hot/heat, cold, freezing, frost) or nutrients deprivation, pollutants stress (heavy metals, toxic chemicals), ozone, high light, pathogen (including viruses, bacteria, fungi, insects and nematodes) and combinations of these.Biotic stress is stress as a result of the impact of a living organism on the plant. Examples are stress caused by pathogens (virus, bacteria, nematodes insects etc..). Another example is stress caused by an organism, which is not necessarily harmful to the plant, such as the stress caused by a symbiotic or an epiphyte.

As shown in Tables 1 and 2, several of the E2Fa-DPa target genes identified have an E2F recognition sequence in their promoter and most of these genes are involved in DNA replication. The secondary induced genes, which are the genes not having the E2F target consensus sequence in their promoter region, encode proteins involved in cell wall biosynthesis, transcription, signal transduction, or have an unknown function. Surprisingly, a large number of metabolic genes were modified as well, mainly genes involved in nitrate assimilation or metabolism and carbon metabolism.

Therefore, according to the invention, there is provided a method as described above, wherein said modified growth characteristic is selected from any one or more of the following: altered development, increased yield and/or biomass, altered plant architecture, altered plant biochemistry, altered plant physiology, altered metabolism, enhanced survival capacity and/or enhanced stress tolerance, each relative to corresponding wild type plants.

The putative direct E2Fa-DPa target genes as identified by the presence of an E2F-DP-binding site, mainly belong to the group of genes involved in DNA synthesis, whereas the secondary induced genes are mainly linked to nitrogen assimilation and carbohydrate metabolism. Therefore, it is elucidated by the present invention that enhanced levels of E2Fa-Dpa in plants have an impact on expression levels of genes involved in nitrogen assimilation. The experimental data suggest that in E2Fa/Dpa overexpressing plants there is a drain of nitrogen to the nucleotide synthesis pathway causing a decreased synthesis of other nitrogen compounds such as amino acids and storage proteins. Corresponding to these findings, the inventors found that that the level of endoreduplication of E2Fa-DPa transgenic plants depends on the amount of nitrogen available in the medium.

As purine and pyrimidine bases are nitrogen-rich, the induction of nitrogen assimilation genes in the E2Fa-DPa transgenic plants is a mechanism to supply enough nitrogen for nucleotide biosynthesis. Most likely this drain of nitrogen from essential biosynthetic pathways to the nucleotide biosynthesis pathway has its effects on many aspects of plant metabolism, as can be seen from the reduction of expression of vegetative storage protein genes and genes involved in amino-acid biosynthesis.

The elucidation of genes that are able to shift the nitrogen assimilation from one biological process to another biological process is important for many applications.

Therefore a particular aspect of the invention is the use of genes involved in carbon and/or nitrogen metabolism or allocation, for altering nitrogen and carbon metabolism and/ or to alter the balance between carbon and nitrogen or to reallocate carbon and/or nitrogen or to alter the composition of components containing carbon and nitrogen. These genes can now be used to alter the nitrogen composition of nitrogen-containing compounds in a cell, such as nicotinamide-containing molecules, amino acid, nucleic acid, chlorophyll or any other metabolites. Also within the scope of the present inventions are these altered components obtainable by the methods of the present invention, with altered balance between carbon and nitrogen. Also envisaged by the present invention is the use of the genes of the present invention, or the proteins as pharmaceutical compounds. Also the genes, proteins and methods as described herein can be used to develop pharmaceutical compounds or to improve known pharmaceutical compounds.

Therefore, according to the present invention, there is provided a method as described above, wherein said altered metabolism comprises altered nitrogen and/or carbon metabolism.

In a particular embodiment, said carbon metabolism comprises the processes of carbon fixation, photosynthesis and photorespiration. In another embodiment, said nitrogen metabolism comprises nitrogen fixation or the reallocation of nitrogen residues from the pool of amino acids into the pool of nucleic acids or vice versa.

Also, a particular embodiment of the present invention is a method as described above to influence DNA synthesis and DNA replication.

Microarray analysis of E2Fa-DPa overexpressing lines identified a cross-talking matrix between DNA replication, nitrogen assimilation and photosynthesis. It has been described previously that here is a link between carbon:nitrogen availability and growth, storage lipid mobilization and photosynthesis (Martin T. (2002)). Therefore according to the present invention there is provided, a method as described above, wherein said altered growth characteristic comprises altered storage lipid mobilization and/or photosynthesis.

The microarray studies elucidated for the first time genes that are upregulated and the genes that are downregulated in a plant cell overexpressing E2Fa/DPa. Accordingly, the present invention provides a recombinant nucleic acid comprising:

(a) one or more nucleic acid sequences essentially similar to a nucleic acid sequence deposited under accession number At1g57680 and/or deposited under any of the

accessions numbers presented in Tables 1, 2, 4 or 5, or the complement thereof; and optionally operably linked to

(b) a regulatory sequence.

In a particular embodiment of the present invention said regulatory sequence is a plant-expressible promoter. In a further embodiment of the invention the promoter is a constitutive promoter, such as the GOS2 promoter, the ubiquitin promoter, the actin promoter. In another embodiment of the invention the promoter is a promoter active in the meristem or in dividing cells, such as, but not limited to the cdc2 promoter, RNR promoter, MCM3 promoter. Alternatively, the regulatory element as mentioned above can be a translational enhancer, or a transcriptional enhancer that is used to enhance the expression of a gene according to the present invention.

The term "Regulatory sequence" refers to control DNA sequences, which are necessary to affect the expression of coding sequences to which they are operably linked. The nature of such control sequences differs depending upon the host organism. In prokaryotes, control sequences generally include promoters, ribosomal binding sites, and terminators. In eukaryotes generally control sequences include promoters, terminators and enhancers or silencers. The term "control sequence" is intended to include, at a minimum, all components the presence of which are necessary for expression, and may also include additional advantageous components and which determines when, how much and where a specific gene is expressed. Reference herein to a "promoter" is to be taken in its broadest context and includes the transcriptional regulatory sequences derived from a classical eukaryotic genomic gene, including the TATA box which is required for accurate transcription initiation, with or without a CCAAT box sequence and additional regulatory elements (i.e. upstream activating sequences, enhancers and silencers) which alter gene expression in response to developmental and/or external stimuli, or in a tissue-specific manner. The term "promoter" also includes the transcriptional regulatory sequences of a classical prokaryotic gene, in which case it may include a -35 box sequence and/or a -10 box transcriptional regulatory sequences.

The term "promoter" is also used to describe a synthetic or fusion molecule or derivative, which confers, activates or enhances expression of a nucleic acid molecule in a cell, tissue or organ. "Promoter" is a DNA sequence generally described as the 5'-region of a gene, located proximal to the start codon. The transcription of an adjacent DNA segment is initiated at the promoter region. In the context of the present invention, the promoter preferably is a plant-expressible promoter sequence. Promoters, however, that also function or solely function in non-plant cells

such as bacteria, yeast cells, insect cells and animal cells are not excluded from the invention. By "plant-expressible" is meant that the promoter sequence, including any additional regulatory elements added thereto or contained therein, is at least capable of inducing, conferring, activating or enhancing expression in a plant cell, tissue or organ, preferably a monocotyledonous or dicotyledonous plant cell, tissue, or organ.

The methods of the present invention are particularly relevant for applications in agriculture and horticulture, and serve to develop plants that have altered growth characteristics. Accordingly, another embodiment of the invention is a method for making a transgenic plant comprising the introduction of a recombinant nucleic acid as mentioned above into a plant.

A further embodiment relates to a method as described above, comprising stably integrating into the genome of a plant a recombinant nucleic acid as mentioned above.

Alternatively, the recombinant nucleic acids comprising the nucleic acids of the present invention are transiently introduced into a plant or plant cell.

The term 'gene(s)' or 'nucleic acid', 'nucleotide sequence', as used herein refers to a polymeric form of a deoxyribonucleotides or ribonucleotide polymer of any length, either double- or single-stranded, or analogs thereof, that have the essential characteristics of a natural ribonucleotide in that they can hybridize to nucleic acids in a manner similar to naturally occurring polynucleotides. A great variety of modifications have been made to DNA and RNA that serve many useful purposes known to those skilled in the art. For example, methylation, 'caps' and substitution of one or more of the naturally occurring nucleotides with an analog. Said terms also include peptide nucleic acids. The term polynucleotide as used herein includes such chemically, enzymatylically or metabolically modified forms of polynucleotides. With "recombinant nucleic acid" is meant a nucleic acid produced by joining pieces of DNA from different sources through deliberate human manipulation.

The inventors identified genes that are upregulated in plants overexpressing E2Fa/DPa. These genes can be used to simulate E2Fa/DPa related effect in a plant.

Therefore, according to the invention, there is provided a method to alter characteristics of a plant, comprising overexpression of one or more nucleic acids essentially similar to a nucleic acid deposited under the accession number At1g57680 and/or deposited under any of the accession numbers presented in Tables 4 or 5, or wherein the method comprises enhancing

the activity of one or more proteins essentially similar to a protein sequence deposited under the accession number At1g57680 and/or deposited under any of the accession numbers presented in Tables 1, 2, 4 or 5.

Also identified were genes that are downregulated in plants overexpressing E2Fa/Dpa. These genes can be used to simulate E2Fa/Dpa related effect in a plant. Therefore, according to the invention, there is provided a method to alter plant growth characteristics, comprising downregulation of the expression of one or more nucleic acids essentially similar to a nucleic acid deposited under the accession number At1g57680 and/or deposited under any of the accession numbers presented in Tables 1, 2, 4 or 5, or wherein the method comprises decreasing the activity of one or more proteins essentially similar to the protein sequence deposited under the accession number At1g57680 and/or deposited under any of the accession numbers presented in Tables 1, 2, 4 or 5.

In the context of the present invention the term "modifying expression" and modifying activity encompasses "enhancing or decreasing". Methods for obtaining enhanced or increased expression of genes or gene products are well documented in the art and are for example overexpression driven by a strong promoter, the use of transcription enhancers or translation enhancers. The term "overexpression" of a gene refers to expression patterns and/or expression levels of said gene normally not occurring under natural conditions. Ectopic expression can be achieved in a number of ways including operably linking of a coding sequence encoding said protein to an isolated homologous or heterologous promoter in order to create a chimeric gene.

Examples of decreasing expression of a gene are also well documented in the art and include for example: downregulation of expression by anti-sense techniques, gene silencing, cosuppression, ribozymes etc.

Modifying the expression of the gene also encompasses altered transcript level of the gene. Altered transcript levels of a gene can be sufficient to induce certain phenotypic effects, for example via the mechanism of cosuppression. Here the overall effect of overexpression of a transgene is that there is less activity in the cell of the protein, which I encoded by the native gene showing homology to the introduced transgene.

Modifying, e.g. increasing or decreasing, the expression of a gene can be achieved for example by respectively inhibiting or stimulating the control elements that drive the expression

of the native gene or of the transgene or recombinant nucleic acid. Also modifying the activity of the protein, the polypeptide or protein, can furthermore be achieved by administering or exposing cells, tissues, organs or organisms to a sample of the protein or to an interacting protein or an inhibitor or activator of the protein. In the context of the present invention, such inhibitors or activators can also affect their activity against the protein of the present invention or to these proteins in the complex with other proteins. In particular, the invention also envisages the modulation of the activity of these proteins by the generation and use of antibodies directed against these proteins.

Further embodiments of the invention relate to a transgenic plant obtainable by any of the methods described above and to a transgenic plant comprising a recombinant nucleic acid sequence essentially similar to a nucleic acid sequence deposited under accession number At1g57680 or deposited under any of the accession numbers presented in Tables 1, 2, 4 or 5, or the complement thereof. Also, another embodiment of the invention relates to an ancestor, progeny, or any plant part, particularly a harvestable part of a transgenic plant as described above.

Detailed analysis of the promoters of the genes identified in the present invention (see Tables 1 or 2) allowed the identification of novel E2Fa/DPa target genes that are under the direct control of E2Fa/Dpa and that are mainly involved in DNA replication. For all the genes identified in the present invention, reference is made to the MIPS database MATDB accession number. This unique identification number refers to the deposit of information related to the gene in question, e.g. the unspliced sequence, the spliced sequence, the protein sequence, the domains of the protein etc. An example of the information deposited under the accession number At1g57680 is shown in figure 4. Based on this unique accession number, a person skilled in the art would know how to locate the gene in its genomic environment and from this information easily identify and isolate the upstream control elements of these genes. Especially interesting are the promoters of these genes as control elements for driving or regulating transcription of heterologous genes. Therefore, according to the invention is provided an isolated nucleic acid comprising one or more of the regulatory elements upstream of the startcodon of the nucleic acids deposited under accession number At1g57680 or deposited under any of the accession numbers presented in Tables 1, 2, 4 or 5. Furthermore, the invention provides an isolated nucleic acid as mentioned above, wherein said regulatory element is the natural promoter of said genes.

Further the invention also relates to the use of a nucleic acid sequence encoding a protein essentially similar to the protein sequence deposited under accession number At1g57680 and/or deposited under any of the accession numbers presented in Tables 4 or 5, or a homologue, a derivative or functional fragment thereof, for altering plant characteristics.

Another method for altering plant characteristics and/or growth characteristics of a plant resides in the use of allelic variants of the genes of the present invention (deposited in the MIPS database under the accession numbers as presented in Tables 1, 2, 4 or 5). Allelic variants exist in nature and encompassed within the methods of the present invention is the use of these natural alleles. Alternatively, in particular conventional breeding programs, such as for example marker assisted breeding, it is sometimes practical to introduce allelic variation in the plants by mutagenic treatment of a plant. One suitable mutagenic method is EMS mutagenesis. Identification of allelic variants then takes place by, for example, PCR. This is followed by a selection step for selection of superior allelic variants of the sequence in question and which give rise to altered growth characteristics. Selection is typically carried out by monitoring growth performance of plants containing different allelic variants of the sequence in question (for example any of the sequences deposited in the database under the accession numbers presented in Tables 1, 2 4 or 5). Monitoring growth performance can be done in a greenhouse or in the field. Further optional steps include crossing plants in which the superior allelic variant was identified with another plant. This could be used, for example, to make a combination of interesting phenotypic features.

According to another aspect of the present invention, advantage may be taken of the nucleic acid sequence encoding a protein of the present invention in breeding programs. In such a program, a DNA marker is identified which is genetically linked to the gene encoding protein of the present invention. This DNA marker is then used in breeding programs to select plants having altered growth characteristics.

Therefore, the present invention also encompass the use of a nucleic acid sequence essentially similar to any one of SEQ ID NO 1 to 52 and/or being essentially similar to the nucleic acid sequence deposited under accession number At1g57680 and/or deposited under any of the accession numbers presented in Tables 1, 2, 4 or 5, or a homologue, a derivative or functional fragment thereof, for marker assisted breeding of plants with altered characteristics.

Further, the present invention also encompass the use of a nucleic acid sequence essentially similar to any one of SEQ ID NO 1 to 52 and/or being essentially similar to the nucleic acid sequence deposited under accession number At1g57680 and/or deposited under any of the accession numbers presented in Tables 1, 2, 4 or 5, or a homologue, a derivative or functional fragment thereof, for conventional breeding of plants with altered characteristics.

Further the invention also relates to the use of a nucleic acid or a protein essentially similar to any one of SEQ ID NO 1 to 104 or a nucleic acid or protein being essentially similar to the nucleic acid or the protein sequence deposited under the accession number At1g57680 or deposited under any of the accession numbers presented in Tables 1, 2, 4 or 5, or a homologue, a derivative or functional fragment thereof, as a growth regulator.
In a particular embodiment such a growth regulator is a herbicide target or is a growth stimulator.

Also the invention as presented here offer means to alter characteristics of not only plants, but also of other organisms such as mammals. The plant genes of the present invention or their homologues, or the plant proteins or their homologues, can be used as therapeutics or can be used to develop therapeutics for both humans and animals. Accordingly, the present invention relates to a nucleic acid or a protein essentially similar to any one of SEQ ID NO 1 to 104 or a nucleic acid or protein being essentially similar to the nucleic acid or the protein sequence deposited under the accession number At1g57680 or deposited under any of the accession numbers presented in Tables 1, 2, 4 or 5, or a homologue, a derivative or functional fragment thereof, for use as a therapeutic agent.
In a particular embodiment, the use as a therapeutic agents encompasses the use in gene therapy, or the use to develop therapeutic protein samples.

Also, the present invention encompasses the use of a protein essentially similar to the protein sequence deposited under the accession number At1g57680 or deposited under any of the accession numbers presented in tables 4 or 5, or a homologue, a derivative or functional fragment thereof, for altering growth characteristics in a plant.

DESCRIPTION OF THE FIGURES

Figure 1: Volcano plot of significance against effect. Each x represent one of the 4579 genes, with the negative log10 of the P value from the gene model plotted against the difference

between least-square means for the genotype effect. The horizontal line represents the test-wise threshold of P=0.05. The two vertical reference lines indicate a 2-fold cutoff for either repression or induction.

Figure 2: Sources of metabolites in plants, with annotation of up and downregulated genes in the E2Fa-DPa overproducing cells. Upregulated enzymes are underlined with a dashed line and enzymes underlined with a full line are downregulated in the E2Fa-DPa versus wild type plants. Products that are boxed act as precursors for nucleotide biosynthesis.

Figure 3: Endoreduplication levels in wild type and E2Fa/DPa transgenic lines in relation to nitrogen availability. Wild type (A) and transgenic (B) lines were grown on minimal medium in the presence of 0.1, 1, 10, or 50 mM ammonium nitrate. Values are means of three independent measurements.

Figure 4: Represents the information which is deposited in the MatDB under accession number At1g57680

Table 1: Presentation of all Arabidopsis genes that are 2 fold or more upregulated in E2Fa/DPa overexpressing plants. The genes are presented according to the functional category to which they belong. For some of the genes, no function has been described in the public databases and they are named unknown, putative or hypothetical protein. All the genes have each a unique MIPS accession number, which refers to the identification of the sequence in the MIPS database (see Example 4). The MIPS accession number refers to the protein entry code for the MatDB of MIPS. Also, there is an accession number provided as an internal protein code. The genes that have been categorized as having a putative function are given a SEQ ID NO. The fold of induction is also given for each sequence. Furthermore, where an E2F target sequence has been identified in the upstream region of the gene, the sequence of that site is also presented in the table. Finally, other plant homologues which have substantial sequence identity with the Arabidopsis gene are mentioned in this table.

Table 2: Presentation of all Arabidopsis genes that are 2 fold or more repressed in E2Fa/DPa overexpressing plants. Data are presented in a similar way as for Table 1, as explained above.

Table 3: Different E2F target sequences and the frequency of their presence in the upstream regions of the Arabidopsis genes described in the present invention.

Table 4: Selection of the Arabidopsis genes from the microarray that were 1.3 times upregulated in E2Fa/Dpa overexpressing plants, compared to the wild–type plants. The gene name is given, as well as the MIPS database accession number (unique identifier, see Example 4) and a ratio indicating the degree of upregulation of the gene. Furthermore, the E-value indicates if a significant homologue has been found in the public databases.

Table 5: Selection of the Arabidopsis genes from the microarray that were 1.3 times repressed in E2Fa/Dpa overexpressing plants, compared to the wild –type plants. The data are presented as in Table 4. The fold repression is calculated as 1/ratio. In this table only the genes that have a ratio of less than 0.77 are selected.

EXAMPLES

Example 1. Overexpression of E2Fa and DPa in Arabidopsis

Double transgenic CaMV35S-E2Fa-DPa plants were obtained by the crossing of homozygous CaMV35S-E2Fa and CaMV35S-DPa plants (De Veylder et al., 2002). Double transformants were grown under a 16h light/ 8h dark photoperiod at 22°C on germination medium (Valvekens et al., 1988).

Selection of transgenic lines

Arabidopsis thaliana plants were generated that contained either the *E2Fa* or the *DPa* gene under the control of the constitutive cauliflower mosaic virus (*CaMV*) *35S* promoter. Out of multiple transgenic lines, two independent *CaMV 35S E2Fa* and two *CaMV 35S DPa*, containing only one T-DNA locus.

Crossing experiments of overexpressing E2Fa and DPa lines

Plants homozygous for the *CaMV 35S E2Fa* gene were crossed with heterozygous *CaMV 35S DPa* lines. Polymerase chain reaction (PCR) analysis on individual plants confirmed which plants contained both the *CaMV 35S-E2Fa* and *CaMV 35S-DPa* constructs.

8 days after sowing, these plants were used to isolate total RNA, from which cDNA was synthesized and subsequently hybridized to a microarray containing 4579 unique Arabidopsis EST's. These experimental steps are described in the following examples.

Example 2: Construction of Microarrays

Construction of Microarrays

The Arabidopsis thaliana microarray consisted of 4,608 cDNA fragments spotted in duplicate, distant from each other, on Type V silane coated slides (Amersham BioSciences, Buckinghamshire, UK). The clone set included 4,579 Arabidopsis genes composed from the unigen clone collection from Incyte (Arabidopsis Gem I, Incyte, USA). To retrieve the functional annotation of the genes relating to the spotted ESTs, BLASTN against genomic sequences was performed. To make the analysis easier a collection of genomic sequences bearing only one gene was built according to the available annotations. Each of those sequences had its upstream intergenic sequence followed by the exon-intron structure of the gene and the downstream intergenic sequence. Here, intergenic means the whole genomic sequence between start and stop codons from neighboring protein-encoding genes. From the BLASTN output we extracted the best hits and submitted them to a BLASTX search against protein databases. To retrieve even more detailed information concerning the potential function of the genes, protein domains were searched using ProDom. The complete set can be found on the website http://www.psb.rug.ac.be/E2F. The cDNA inserts were PCR amplified using M13 primers, purified with MultiScreen-PCR plate (cat: MANU03050, Millipore, Belgium) and arrayed on the slides using a Molecular Dynamics Generation III printer (Amersham BioSciences). Slides were blocked in 3.5%SSC, 0.2%SDS, 1%BSA for 10 minutes at 60°C.

RNA amplification and labeling

Antisense RNA amplification was performed using a modified protocol of in vitro transcription as described earlier in Puskas et al. (2002). For the first strand cDNA synthesis, 5 µg of total RNA was mixed with 2 µg of a HPLC-purified anchored oligo-dT + T7 promoter (5'-GGCCAGTGAATTGTAATACGACTCACTATAGGGAGGCGG-T_{24}(A/C/G)-3') (SEQ ID NO 105). (Eurogentec, Belgium), 40 units of RNAseOUT (cat# 10777-019, Invitrogen, Merelbeke, Belgium) and 0.9M D(+) trehalose (cat# T-5251, Sigma Belgium) in a total volume of 11µl, and heated to 75°C for 5 minutes. To this mixture, 4 µl 5x first strand buffer (Invitrogen,, Belgium), 2 l 0.1 M DTT, 1 µl 10 mM dNTP mix, 1 µl 1.7 M D(+)trehalose (cat# T-5251, Sigma Belgium) and 1 µl, 200 Units of SuperScript II (cat#: 18064-014, Invitrogen, Belgium) was added in 20 µl final volume. The sample was incubated in a Biometra-UnoII thermocycler at 37°C for 5 minutes, 45°C for 10 minutes, 10 cycles at 60°C for 2 minutes and at 55°C for 2 minutes. To the first strand reaction mix, 103.8 µl water, 33.4 µl 5x second strand synthesis buffer (Invitrogen, Belgium), 3.4 µl 10 mM dNTP mix, 1 µl of 10U/µl E.coli DNA ligase (cat#: 18052-019, Invitrogen, Belgium), 4 µl 10 U/µl E.coli DNA Polymerase I (cat#: 18010-025, Invitrogen, Belgium) and 1 µl 2U/µl E.coli RNAse H (cat#: 18021-071, Invitrogen, Belgium) was added, and incubated at 16°C for 2 hours. The synthesized double-stranded cDNA was purified with Qiaquick (cat#: 28106, Qiagen, Hilden, Germany). Antisense RNA synthesis was done by

AmpliScribe T7 high yield transcription kit (cat#: AS2607; Epicentre Technologies, USA) in total volume of 20 µl according to the manufacturer's instructions. The RNA was purified with RNeasy purification kit (cat#: 74106; Qiagen, Germany). From this aRNA, 5 µg was labeled by reverse transcription using random nonamer primers (Genset, Paris, France), 0.1 mM d(G/T/A)TPs, 0.05 mM dCTP (Amersham BioSciences, UK), 0.05 mM Cy3-dCTP or Cy5-dCTP (cat#: PA53023, PA55023; Amersham BioSciences, UK) 1x first strand buffer, 10 mM DTT and 200 Units of SuperScript II (cat#: 18064-014, Invitrogen, Belgium) in 20 µl total volume. The RNA and primers were denatured at 75°C for 5 minutes and cooled on ice before adding the remaining reaction components. After 2 hours incubation at 42°C, mRNA was hydrolyzed in 250 mM NaOH for 15 minutes at 37°C. The sample was neutralized with 10 µl of 2 M MOPS and purified with Qiaquick (cat#: 28106, Qiagen, Germany).

Array hybridization and post-hybridization processes

The probes were resuspended in 30 µl hybridization solution (50 % formamide, 5x SSC, 0.1 % SDS, 100 mg/ml salmon sperm DNA) and prehybridized with 1µl poly-dT (1mg/ml) at 42°C for 30 minutes to block hybridization on the polyA/T tails of the cDNA on the arrays. 1 mg/ml mouse COT DNA (cat#: 18440-016, Invitrogen, Belgium) was added to the mixture and placed on the array under a glass coverslip. Slides were incubated for 18 hours at 42°C in a humid hybridization cabinet (cat#: RPK0176; Amersham BioSciences, UK). Post-hybridization washing were performed for 10 minutes at 56°C in 1xSSC, 0.1% SDS, two times for 10 minutes at 56°C in 0.1xSSC, 0.1% SDS and for 2 minutes at 37°C in 0.1xSSC.

Scanning and data analysis

Arrays were scanned at 532 nm and 635 nm using a Generation III scanner (Amersham BioSciences, UK). Image analysis was performed with ArrayVision (Imaging Research Inc, Ontario, Canada). Spot intensities were measured as artifact removed total intensities (ARVol). No background correction was performed. We first addressed within-slide normalization by plotting for each single slide a "MA-plot" (Yang et al., 2002), where $M = \log_2 (R/G)$ and $A = \log_2 0.5\sqrt{R \times G}$. The "LOWESS" normalization was applied to correct for dye-intensity differences. Subsequently, in order to normalize between slides and to identify differentially expressed genes between the two genotypes, we applied two sequential analyses of variance (ANOVAs), proposed by Wolfinger et al. (2002), as follows: 1) firstly, we subjected the base-2 logarithm of the "LOWESS"-transformed measurements for all 73,264 spots (y_{gklm}) to a normalization model of the form $y_{iklm} = \mu + A_k + A_k D_l R_m + \varepsilon_{iklm}$, where μ is the sample mean, A_k is the effect of the kth array (k = 1-4), $A_k D_l R_m$ is the channel-effect (AD) for the mth replication of the total collection of cDNA fragments (m = 2; left or right), and ε_{iklm} is the stochastic error; 2) secondly, we then

subjected the residuals from this model to 4,579 gene-specific models of the form $r_{ijkl} = \mu + G_iA_k + G_iD_l + G_iC_j + \gamma_{ijkl}$ where G_iA_k is the spot effect, G_iD_l is the gene-specific dye effect, G_iC_j is representing the signal intensity for genes that can specifically be attributed to the genotypes (effect of interest), and γ_{ijkl} is the stochastic error. All effects were assumed to be fixed effects, except ε_{klm} and γ_{ijkl}. We t-tested for differences between the G_iC_j effects, where the t-tests are all based on n_1+n_2-2 degrees of freedom corresponding to the n_1 WT hybridisations and n_2 E2Fa-DPa hybridisations. The p-value cutoff was set at 0.01. No further adjustment for multiple testing was performed, as Bonferroni adjustment for 4,579 tests, to assure an experiment-wise false positive rate of 0.05, results in a p-value cutoff of $1e^{-5.0}$, which is certainly too conservative; we therefore choose to set our p-value cutoff arbitrarily at the 0.01 level. Also G_iD_l effects were estimated and t-tested for significance at the 1% level in a same way as described above. Genes with a significant G_iD_l effect were discarded. We used Genstat to perform both the normalization and gene model fits.

Example 3: Results of the Microarray analysis and statistical analysis

A micro-array containing in duplo 4579 unique Arabidopsis ESTs, representing about a sixth of the total genome, was used to compare the transcriptome of wild type with that of *E2Fa-DPa* overexpressing plants. cDNA was synthesized from total RNA isolated from wild type and transgenic plants harvested 8 days after sowing. At this stage transgenic plants can be distinguished from control plants by the appearance of curled cotelydons which display ectopic cell divisions and enhanced endoreduplication (De Veylder et al., 2002). In first two hybridizations Cy3 and Cy5 fluorescently labeled probe pairs of control and *E2Fa-DPa* cDNA were used, using independent mRNA extractions of the *E2Fa-DPa* plants. Subsequently, a dye-swap replication was performed for both hybridizations, resulting in a total of four cDNA microarray hybridizations.

Fluorescence levels were analyzed with the aim to establish whether the level of expression of each gene varies according to the overexpression of the *E2Fa-DPa* transcription factor. Two sequential analyses of variance (ANOVAs) were used, as proposed by Wolfinger et al. (2002). The first ANOVA model, called the "normalization"model, accounts for experiment-wise systematic effects, such as array- and channel-effects, that could bias inferences made on the data from the individual genes. The residuals from this model represent normalized values and are the input data for the second ANOVA model, called the "gene" model. The gene models are fit separately to the normalized data from each gene (see M&M). This procedure uses differences in normalized expression levels, rather than ratios, as the unit of analysis of expression differences.

Prior to the estimation of genotype-specific signal intensities of the genes (G_iC_j effects), which are the effects of interest, gene-specific dye effects (G_iD_j effects) were estimated and t-tested for significance at the 1% level. One hundred thirty one genes showed a significant G_iD_j effect and were discard from further analysis. For each of the remaining 4,448 genes on the arrays, we t-tested the G_iC_j effects for significant differences ($p<0.05$). Figure 1 plots the obtained p-values (as the negative log10 of the p-value) against the magnitude of the effect (log2 of estimated fold change). This volcano plot illustrates the substantial difference significance testing can make versus cutoffs made strictly on the basis of the fold change. The two vertical reference lines indicate a 2-fold cutoff for either repression or induction, while the horizontal reference line refers to the p-value cutoff at the 0.05 value. These references lines divide the plot into six meaningful sectors. The 3,535 genes in the lower middle sector have low significance and low fold change, and both methods agree that the corresponding changes are not significant. The 188 genes in the upper left and right sectors have high significance ($p<0.05$) and high fold change (≥ 2); 84 of these genes show a significant two-or-more-fold induction of expression, where the remaining 104 genes show a significant two-or-more-fold repression of expression in the E2Fa-DPa plant. Finally, the 715 genes in the upper middle sector represent significant ($p<0.05$) up- or downregulated genes, but with a low (≤ 2) fold change. The full dataset of genes can be viewed at http://www.psb.rug.ac.be/E2F.

Example 4: Characterization of the genes identified as being involved in E2F/DP regulated cellular processes

All the sequences that are 1.3 times upregulated (ratio of more than 1.999) in E2Fa/Dpa overexpressing plants are presented in Table 4. All the sequences that are 1.3 times repressed (calculated as 1/ ratio of less than 0.775) are presented in Table 5. Particular interesting genes that are more than 2-fold upregulated or 2 fold repressed are selected and separately represented in Tables 1 and 2.

As mentioned in Example 2, the genes from the microarray are characterized by their unique identification number (MIPS accession number e.g. At1g57680). The MIPS accession number is widely accepted in this field as it directly refers to the genomic sequence and the location of the sequence in the Arabiodpsis thaliana genome. Accession numbers are allocated by the Munich Information Center for Protein Sequences (MIPS) and are stored in the MIPS Arabidopsis database. Publicly available sequence and annotation data from all other AGI ("Arabidopsis Genome Initiative") groups are included to establish a plant genome database (Schoof H, et al. (2002)). The MIPS Arabidopsis database can be accessed via the internet

http://mips.gsf.de/cgi-bin/proj/thal and the database can be searched with the protein entry code (e.g. At1g57680). An example of the type of sequence information and protein domain information that is provided for a certain sequence in the MIPS database, is shown Figure 4.

Further, with the gene an additional blast search was performed on public databases also containing sequences of other plant species or other organisms. For some of the genes identified by the microarray, significant levels of homology (low E-values) were found with sequences from other organisms and these were also mentioned in the Tables 1 and 2. The E-values of Tables 1, 2, 4 or 5 give an indication if significant homologues are found or not. For the unknown proteins an E-value of 0 means that no functional homologues was found yet.

DNA replication and cell cycle genes

Genes up or downregulated in the *E2Fa-DPa* transgenics can be classified into clear groups according their function (Tables 1 and 2). Among the genes being 2-fold or more upregulated belong 13 to the class of DNA replication and modification, correlating with the observation that E2Fa-DPa overexpression plants undergo extensive endoreduplication. Most of these genes have previously be shown to be upregulated by *E2F-DP* overexpression in mammalian systems including a putative thymidine kinase, replication factor c, and histone genes (4 different ones). Other E2Fa-DPa induced S phase genes include a linker histone protein, the topoisomerase 6 subunit A and two subunits of the histone acetyltransferase HAT B complex, being HAT B and Msi3. The HAT B complex is responsible for the specific diacethylation of newly synthesized histone H4 during nuclease assembly on newly synthesized DNA (Less et al., 1999). Also a DNA methyltransferase responsible for the methylation of cytosine in cells that progress though S phase can be identified among upregulated genes.

Besides the overexpressed E2Fa gene (being 90-fold more abundant in the transgenic plants, compared to control plants), only one cell cycle gene (*CDKB1;1*) shows a 2-fold or more change in expression level upon *E2Fa-DPa* overexpression. CDKB1;1 was already predicted before to be a candidate E2F-DP target by the presence of a consensus E2F-DP-binding site in its promoter (de Jager et al., 2001). Whereas CDKB1;1 activity is maximum at the G2/M transition, its transcript levels start to rise during late S-phase (Porceddu et al., 1996; Menges and Murray, 2002). Upregulation of *CDKB1;1* might therefore be a mechanism to link DNA replication with the following mitosis. The lack of detection of other cell cycle genes being modulated in the E2Fa-DPa plants can be explained by the lack of many important E2F-DP target genes on the microarray and the putative difficulty to detect changes in expression levels of low abundantly expressed genes by the microarray technique.

Cell wall biogenesis genes

Four members of the xyloglucan endotransglucosylase (XET) gene family can be found to be 2-fold or more upregulated in the E2Fa-DPa plants, one of them identical to the Meri-5 gene (Medford et al., 1991). XETs are enzymes that modify cell wall components and play a very likely role in altering the size, shape and physical properties of plant cells. Reversal breakage of the xyloglucan tethers by XETs has been proposed to be a mechanism for allowing cell wall loosening in turgor-driven cell expansion (Campbell and Braam, 1999). However, there are several reasons to believe that E2Fa-DPa induced XETs are not required for cell expansion. First, cells divide more frequently in the E2Fa-DPa plants, but the overall cell size is smaller in the transgenic than control plants, so no overall increase in expansion rates is needed. Second, correlated with the absence of increased cell expansion in the transgenic lines no induction can be seen of genes with a known role in this process, such as expansins. Therefore, the hydrolytic activity of the XETs might rather be required to incorporate the newly synthesized cell walls formed during cytokinesis into the existing cell wall structure. Alternatively, as XET activity has shown to be involved in the postgerminative mobilization of xyloglucan storage reverses in Nasturtium cotelydons (Farkas et al., 1992; Fanutti et al., 1993), induction of XETs in E2Fa/DPa plants might relate to polysaccharide breakdown to serve the metabolic and energy needs which are required to synthesize new nucleotides (see below).

Interestingly, two XETs can be identified in the set of 2-fold or more downregulated genes. These XETs are more related to each other than to the induced XET proteins. This differential response of XETs towards the E2Fa/DPa induced phenotypes suggests that plant XETs can be classified in at least 2 different functional classes.

Genes involved in metabolism and biogenesis

Both the group of up and down regulated genes contain a relative large group of genes involved in metabolism and biogenesis. Most remarkable is the induction of genes involved in nitrogen assimilation, such as nitrogen reductase, glutamine synthetase (GS), and glutamate synthetase (GOGAT). Nitrogen reductase catalyses the first step in the nitrogen assimilation pathway, whereas glutamine and glutamate synthetase are involved in both the primary assimilation from nitrogen as reassimilation of free ammonium, supplying all plants nitrogen needed for the biosynthesis of amino-acids and other nitrogen-containing compounds. Upregulation of nitrogen assimilation genes in the E2Fa-DPa transgenic plants might reflect

the need for nitrogen for nucleotide biosynthesis, as purine and pyrimidine bases are nitrogen-rich.

There are other indications that the nitrogen metabolism is altered in the E2Fa-DPa plants, such as the modification of genes reported to be involved in Medicago induced nodulation (MTN3 and a nodulin-like gene); and the downregulation of genes involved in sulfur assimilation (adenylylsulfate reductase (APR; 2 different genes) and a putative adenine phosphosulfate kinase). Genes involved in sulfur assimilation such as APR have been shown before to transcriptionally downregulated during nitrogen deficiency (Koprivova et al., 2000).

Nitrogen assimilation through the GS/GOGAT pathway requires α-ketogluterate (Lancien et al., 2000). Our micro-array data suggest that in the *E2Fa-DPa* overexpressing plants α-ketogluterate accumulation is stimulated in different ways. First, α-ketogluterate production is improved by increased photosynthetic activity, as indicated by the 4.7-fold upregulation of large subunit of ribulose-1,5-bisphosphate carboxylase/oxygenase (Figure 2). This will results in an accumulation of glyceraldehyde-3-phosphate. Glyceraldehyde-3-phosphate can be converted into fructuse-1,6-bisphosphate by fructose bisphosphate aldolase. However, a 6-fold downregulation of the fructose bisphosphate aldolase gene rather suggests the conversion of glyceraldehyde-3-phosphate into pyruvate, which can be converted into α-ketogluterate during glycolysis in the citrate cycle. The preferential conversion of glyceraldehyde-3-phosphate into pyruvate in favour of sugars fit the higher need for amino-acids than for sugars for nucleotide biosynthesis. A shortage for ribose-5-phosphate for nucleotide synthesis is also evident from a downregulation of sucrose-phosphate synthase, resulting in a decreased conversion of fructose-6-phosphate and glucose-6-phosphate into sucrose (Figure 2).

A second source of α-ketogluterate is provided in the glyoxylate cycle by the 3.1 fold increase in expression of isocitrate lyase, suggesting an increased lipid turnover in the E2Fa-DPa plants. Isocistrate lyase activity cleaves isocitrate into glyoxylate and succinate (figure 2). Whereas the formed glyoxylate can be converted into glycine, which is also required for nucleotide biosynthesis, can succinate be converted into α-ketogluterate in the citrate cycle. A 2.3-fold decrease of the fumarase gene presumably stimulates the conversion of produced α-ketogluterate into glutamate by causing an accumulation of succinate and fumarate, which is also a side product formed during nucleotide biosynthesis (Figure 2).

Assimilation of nitrogen is energy consuming. When rates of nitrate reduction are high, this pathway becomes the major sink for reductant. About 10% of the electron flux in

photosynthesizing leaves is used for nitrate reduction. The amount of required reductant, which in leaves originates from electronic photosynthetic electron transport, is therefore expected to be higher in the E2Fa-DPa transgenics. Correspondingly, several components of the chloroplast electron transport chain and associated ATP-synthesing apparatus, such as cytochrome B6, a PSII subunit and the ATPase epsilon subunit are upregulated in the transgenic plants. Increased expression of the protochlorophyllide reductase precursor suggests that an increase in chlorophyll biosynthesis is stimulated in the E2Fa-DPa plants. Famine of nitrogen has a putative impact on amino-acid biosynthesis, as three different amino-acid aminotransferases, are downregulated in the E2Fa-DPa plants. Accompanied with a putative decreased aminotransferase activity is the observed reduction in expression of an enzyme involved in pyridoxine biosynthesis. Shortage of nitrogen-rich amino-acids is also evident from reduced expression of the genes encoding vegetative storage proteins (VSP1and VSP2); and ERD10, a protein with a compositional bias towards glu (Kiyosue et al., 1994). Additional evidence for amino acid shortage comes from the downregulation of a myrosinase-binding protein and the cytochrome P450 monooxygenase CYP83A1. Both proteins are involved in the biosynthesis of glucosinolates, being nitrogen and sulfur containing products derived from amino-acids (Wittstock and Halkier, 2002).

Transcription factors and signal transduction

A total of 4 transcription factors were identified among the genes being 2-fold or more upregulated, including two homeobox domain transcription factors. Among them we identified the anthocyaninless2 (ANL2) gene, involved in anthocyanin accumulation in subepidermal leaf cells (Kubo et al., 1999). The lack of an obvious increase in anthocyanin accumulation in the E2Fa-DPa plants suggests a role for the ANL2 protein in plant development different from anthocyanin production. This hypothesis is substantiated by the observation that anl2 mutant plants contain extra cells in the root between the cortical and epidermal layers (Kubo et al., 1999).

The second upregulated homebox domain transcription factor is Atbh-6. Expression of Atbh-6 is restricted to regions of cell division and/or differentiation, and has been shown to to be inducible by water stress and ABA (Soderman et al., 1999). Other putative ABA sensitive genes can be recognized among the E2Fa-DPa induced clones as well including the cold regulated protein COR6.6, a seed imbitition-like protein, and a dormancy-associated protein. Here again, changes in the expression level of these genes might be correlated with modifications in carbon metabolism. A link between ABA and sugar signaling is evident from the identification of several loci involved in both sugar and hormonal responses (Finkelstein

and Gibson, 2002). Alternatively, it might be the occurrence of enhanced endoreduplication and/or cell division itself that causes a change in the osmotic potential.

Among the downregulated transcription factors a DOF family member is present. Many DOF transcription factors are participating in the regulation of storage protein genes and genes involved in carbon metabolism (Gualberti et al., 2002). Its downregulation might therefore be linked with the shortage of amino-acids due to the high demand of nitrogen for nucleotide biosynthesis.

Other regulatory genes modified in the E2Fa-DPa plants include protein kinases, several putative receptor kinases, a putative phytochrome A, and WD-40 repeat containing proteins (Tables 1 and 2). Interestingly, a SNF1-like kinase is downregulated 2-fold in the E2Fa-DPa plants. In addition to its proposed role in sugar signaling, the SNF1 kinase also regulates negatively the activity of plant nitrate reductase (Smeekens, 2000).

Endoreduplication levels of E2Fa-DPa plants are nitrogen dependent

The modified expression of a large number of metabolic and regulatory genes directly or indirectly linked to nitrogen metabolism suggests a direct relationship between the high endoreduplication levels found in the E2Fa/DPa transgenic plants and nitrogen availability. To test this hypothesis, wild type and transgenic plants were grown on medium containing different levels of ammoniumnitrate, ranging from 0.1 to 50 mM. Eight days after germination the ploidy levels in these plants were determined by flow cytometry. Increasing ammoniumnitrate levels hardly had an effect on the ploidy distribution pattern in wild type plants (figure 3A). In contrast, in the E2Fa-DPa transgenic plants increasing ammoniumnitrate levels resulted in a reproducible and significant increase in the amount of 32C and 64C nuclei (figure 3B). Comparing the lowest with the highest concentration of ammonimumnitrate an increase of 32C from 2.0 (± 0.3) % to 6.5 (± 1.5) %, and of 64C from 0.7 (±0.3) % to 2 (± 0.5) % can be seen. Increasing ammonium levels did not have any effect on the plant phenotype, as plants remained small with curled leaves on all concentrations of nitrogen tested. These data indicate that the endoreduplication levels in the E2Fa/DPa plants are limited by nitrogen availability, and that an excess of nitrogen is rather incorporated into new DNA than other nitrogen containing compounds.

Example 5: Promoter analysis of E2Fa-DPa regulated genes

Promoter analysis

The intergenic sequence corresponding to the promoter area of each gene spotted on the microarray was extracted from genomic sequences. These genomic sequences are easily accessible for example from the MIPS MatDB database (http://mips.gsf.de/proj/thal/db/). From those intergenic sequences up to 500bp upstream of the ATG start codon were extracted and subjected to motif searches in order to retrieve potential E2F elements. Both the position and frequency of occurrence were determined using the publicly available executable of MatInspector (version 2.2) using matrices extracted from PlantCARE and matrices made especially for this particular analysis (Lescot et al., 2002). The relevance of each motif was evaluated against a background consisting of all the sequences from the dataset.

Results

To distinguish in our data set the putative direct target genes of E2Fa-DPa from the secondary induced genes, the first 500 bp upstream of the ATG start codon of the genes with 2-fold or more change in expression was scanned for the presence of a E2F-like binding site matching the sequence (A/T)TT(G/C)(G/C)C(G/C)(G/C). Of all different permutations only the TTTCCCGC element was statistically enriched in the set of E2Fa-DPa upregulated genes, suggesting it is the preferred binding site of the E2Fa-DPa complex (Table 3). Moreover, target genes containing this element belong mainly to the group of genes involved in DNA replication and modification, being the main group of target genes in mammalian systems. These data illustrate that the TTTCCCGC sequence is the most likely cis element recognized by E2Fa-DPa. The observation that not all genes having this DNA sequence in their promoter suggests that the presence of the TTTCCCCGC motif is not sufficient to make a gene responsive towards E2Fa-DPa, and that E2Fa-DPa co-operates with other factors to activate transcription. In the Nicotiana benthamiana PCNA promoter a E2F sequence was identified acting as a negative regulatory element during development (Egelkrout et al., 2001). Also the tobacco ribonucleotide reductase small subunit gene contains a E2F element working as a repressor outside the S-phase (Chaboute et al., 2000). In the set of downregulated genes no particular enrichment of a specific E2F sequence could be seen (Table 3). Therefore we believe that the E2Fa-DPa complex mainly works as a transcriptional activator, and that other E2F-DP complexes are involved in E2F-mediated transcriptional repression.

Example 6: Individual characterization of some genes identified by the method of the present invention

At1g07000 showing homology to leucine zipper

At1g07000 is a potential leucine zipper that is not preceded by a basic domain. The leucine zipper consists of repeated leucine residues at every seventh position and mediates protein dimerization as a prerequisite for DNA-binding. The leucines are directed towards one side of an alpha-helix. The leucine side chains of two polypeptides are thought to interdigitate upon dimerization (knobs-into-holes model). The leucine zipper may dictate dimerization specificity. Leucine zippers are DNA binding protein with dimerization properties, having important functions in development and stress tolerance in plants.

At1g09070 showing homology to Soybean Cold Regulate gene SRC2

This genes and its expressed protein is predicted in Arabidopsis, rice, corn, soybean, however, based on a homology search using the BLAST program, no functional homologue known, not even a clear animal homologue, so no clear function can be predicted for this gene or protein (Takahashi,R. and Shimosaka,E. (1997)).

At1g21690 showing homology to Replication factor

Replication factor C (RFC) is a pentameric complex of five distinct subunits that functions as a clamp loader, facilitating the loading of proliferating cell nuclear antigen (PCNA) onto DNA during replication and repair. More recently the large subunit of RFC, RFC (p140), has been found to interact with the retinoblastoma (Rb) tumor suppressor and the CCAAT/enhancer-binding protein alpha (C/EBPalpha) transcription factor. It is reported that RFC (p140) associates with histone deacetylase activity and interacts with histone deacetylase 1 (HDAC1) (Anderson, L. A. and Perkins, N. D. (2002); Furukawa,T. et al. (2001)) RFC is poorly known in plants, can be important for development for modulating gene expression during cell cycle at S phase, or through chromatin regulation.

At1g23030 showing homology to Armadillo protein

Members of the armadillo (arm) repeat family of proteins are implicated in tumorigenesis, embryonic development, and maintenance of tissue integrity. ARM proteins participate in linking cytoskeleton to membrane proteins and structures. These proteins share a central domain that is composed of a series of imperfect 45 amino acid repeats. Armadillo family members reveal diverse cellular locations reflecting their diverse functions. A single protein exerts several functions through interactions of its armadillo repeat domain with diverse binding partners. The proteins combine structural roles as cell-contact and cytoskeleton-

associated proteins and signaling functions by generating and transducing signals affecting gene expression. The study of armadillo family members has made it increasingly clear that a distinction between structural proteins on the one hand and signaling molecules on the other is rather artificial. Instead armadillo family members exert both functions by interacting with a number of distinct cellular-binding partners. Proteins of the armadillo family are involved in diverse cellular processes in higher eukaryotes. Some of them, like armadillo, beta-catenin and plakoglobins have dual functions in intercellular junctions and signalling cascades. Others, belonging to the importin-alpha-subfamily are involved in NLS recognition and nuclear transport, while some members of the armadillo family have as yet unknown functions. (Wang, Y. X. et al. (2001); Hatzfeld, M. (1999). ARM proteins are key protein binding units that are involved at several steps during development. Some are specific of cell cycle, APC degradation complex. These type of genes have been poorly studied in plants, some have been involved in light and gibberellin signaling in potato.

At1g27500 showing homology to Kinesin light chain.

The motor protein kinesin is a heterotetramer composed of two heavy chains of approximately 120 kDa and two light chains of approximately 65 kDa protein. Kinesin motor activity is dependent on the presence of ATP and microtubules. Conventional kinesin is prevented from binding to microtubules (MTs) when not transporting cargo. The function of LC kinesin is to keep kinesin in an inactive ground state by inducing an interaction between the tail and motor domains of HC; activation for cargo transport may be triggered by a small conformational change that releases the inhibition of the motor domain for MT binding. This protein is important to regulate movement controlled by microtubules within the cytoplasm, for example the flux of vesicles between the different cell membrane compartments.

At1g72180 showing homology to Putative receptor protein kinase

Plant receptor-like kinases (RLKs) are transmembrane proteins with putative amino-terminal extracellular domains and carboxyl-terminal intracellular kinase domains, with striking resemblance in domain organization to the animal receptor tyrosine kinases such as epidermal growth factor receptor. The recently sequenced Arabidopsis genome contains more than 600 RLK homologs. Although only a handful of these genes have known functions and fewer still have identified ligands or downstream targets, the studies of several RLKs such as CLAVATA1, Brassinosteroid Insensitive 1, Flagellin Insensitive 2, and S-locus receptor kinase provide much-needed information on the functions mediated by members of this large gene family. RLKs control a wide range of processes, including development, disease resistance,

hormone perception, and self-incompatibility. Combined with the expression studies and biochemical analysis of other RLKs, more details of RLK function and signaling are emerging.

At1g72900 showing homology to Disease resistance protein (TIR virus resistance protein)

This gene has been described by Kroczynska, B. et al. (1999)

At2g30590 showing homology to WRKY transcription factor (Toll/interleukin-1 receptor-like protein)

This sequence shows homology to tomato Cf-9 resistance gene Avr9/Cf-9 rapidly elicited protein 4 (NL27) (Hehl, R. et al. (1998))

At1g80530 showing homology to Nodulin

Infection of soybean roots by nitrogen-fixing Bradyrhizobium japonicum leads to expression of plant nodule-specific genes known as nodulins. Nodulin 26, a member of the major intrinsic protein/aquaporin (AQP) channel family, is a major component of the soybean symbiosome membrane (SM) that encloses the rhizobium bacteroid. These results indicate that nodulin 26 is a multifunctionalAQP that confers water and glycerol transport to the SM, and likely plays a role in osmoregulation during legume/rhizobia symbioses. (Dean et al. (1999). Rice (Oryza sativa var. Nipponbare) possesses two different homologues of the soybean early nodulin gene GmENOD93 (GmN93), OsENOD93a (homology of 58.2% to GmENOD93), OsENOD93b (homology of 42.3%). In intact rice tissues, OsENOD93b was most abundantly expressed in roots and at much lower levels in etiolated and green leaves, whereas the expression of OsENOD93a was very low in roots and etiolated leaves, and was not detected in green leaves. The level of OsENOD93a expression was enhanced markedly in suspension-cultured cells, whereas that of OsENOD93b did not increase (Reddy et al. (1998)). Homologues of genes that are produced in response to infection of soybean roots by bacteria are also present in other plants such rice. Their function is largely unknown, some functional homologues are identified such as a water channel involved in osmoregulation.

At2g34770 showing homology to Fatty acid hydroxylase

This gene has been described in Matsuda et al. (2001). A common feature of the membrane lipids of higher plants is a large content of polyunsaturated fatty acids, which typically consist ofdienoic and trienoic fatty acids. Two types of omega-3 fatty acid desaturase, which are present in the plastids and in the endoplasmic reticulum (ER), respectively, are responsible for the conversion of dienoic to trienoic fatty acids. To establish a system for investigating the

tissue-specific, and hormone-regulated expression of the ER-type desaturase gene (FAD3), transgenic plants of Arabidopsis thaliana (L.) Heynh. containing the firefly luciferase gene (LUC) fused to the FAD3 promoter (FAD3::LUC) were constructed. The results from this study suggest that the expression of ER-type desaturase is regulated through synergistic and antagonistic hormonal interactions, and that such hormonal regulation and the tissue specificity of the expression of this gene are further modified in accordance with the growth phase in plant development (Wellesen K. et al. (2001); Kachroo P. et al. (2001); Kahn, R. A. et al. (2001); Smith, M. et al. (2000).

At2g43402 showing homology to Cinnamoyl CoA reductase

CCR enzyme is involved in lignification. The CCR transcript is expressed in lignified organs, i.e. root and stem tissues, and is localized mainly in young differentiating xylem. Also, monolignols may be precursors of end products other than lignins. CCR catalyses the conversion of cinnamoyl-CoAs into their corresponding cinnamaldehydes, i.e. the first step of the phenylpropanoid pathway specifically dedicated to the monolignol biosynthetic branch. The two genes are differentially expressed during development and in response to infection. AtCCR1 is preferentially expressed in tissues undergoing lignification. In contrast, AtCCR2, which is poorly expressed during development, is strongly and transiently induced during the incompatible interaction with Xanthomonas campestris pv. Campestris leading to a hypersensitive response. Altogether, these data suggest that AtCCR1 is involved in constitutive lignification whereas AtCCR2 is involved in the biosynthesis of phenolics whose accumulation may lead to resistance.(Lauvergeat et al. (2001). This protein is involved during development, increase in growth diameter, lignification of vascular strands and interfascicular fibers.

At2g47440 showing homology to Tetratricopeptide repeat protein

The tetratricopeptide repeat (TPR) is found in a many proteins performing a wide variety of functions, the TPR domain itself is believed to be a general protein recognition module. Different proteins may contain from 3 to 16 tandem TPR motifs (34 amino acid sequence). It has been shown that some proteins contain a TPR repeat are cell cycle regulated.

At3g23750 showing homology to Receptor like kinase TMK

The kinase domain of NtTMK1 contained all of 12 subdomains and invariant amino acid residues found in eukaryotic protein kinases. The extracellular domain contained 11 leucine-rich repeats which have been implicated in protein-protein interactions. The amino acid sequence of NtTMK1 exhibited high homology with those of TMK1 of Arabidopsis and TMK of

rice in both kinase and extracellular domains, suggesting that NtTMK1 is a TMK homologue of tobacco. The NtTMK1 transcripts were present in all major plant organs, but its level varied in different developmental stages in anthers and floral organs. NtTMK1 mRNA accumulation in leaves was stimulated by CaCl2, methyl jasmonate, wounding, fungal elicitors, chitins, and chitosan. The NtTMK1 mRNA level also increased upon infection with tobacco mosaic virus (Cho and Pai (2000). This protein is involved in different aspects of development and disease resistance.

At3g61460 showing homology to RING H2

RING-finger proteins contain cysteine-rich, zinc-binding domains and are involved in the formation of macromolecular scaffolds important for transcriptional repression and ubiquitination. RING H2 act as E3 ubiquitin-protein ligases and play critical roles in targeting the destruction of proteins of diverse functions in all eukaryotes, ranging from yeast to mammals. Arabidopsis genome contains a large number of genes encoding RING finger proteins. A small group is constituted by more than 40 RING-H2 finger proteins that are of small size, not more than 200 amino acids, and contain no other recognizable protein-protein interaction domain(s). This type of genes is very important for several aspect of development, regulation of developmental proteins, cell cycle proteins.

At4g00730 showing homology to Homeodomain AHDP (antocyaninless 2)

This is a homeodomain transcription factor; similar to ATML1 and is very conserved and has epidermis specific expression. This sequence shows also homology to Zea mays mRNA for OCL3 protein (Ingram, G. C. et al. (2000)).

At4g13940 showing homology to adenosylhomocysteinase (Glutathione dependent formaldehyde dehydrogenase)

Glutathione-dependent formaldehyde dehydrogenase was described in Sakamoto, A. et al. (2002), Arabidopsis glutathione-dependent formaldehyde dehydrogenase is an S-nitrosoglutathione reductase. S-Nitrosoglutathione (GSNO), an adduct of nitric oxide (NO) with glutathione, is known as a biological NO reservoir. Heterologous expression in Escherichia coli of a cDNA encoding a glutathione-dependent formaldehyde dehydrogenase of Arabidopsis thaliana showed that the recombinant protein reduces GSNO. The identity of the cDNA was further confirmed by functional complementation of the hypersensitivity to GSNO of a yeast mutant with impaired GSNO metabolism. This is the first demonstration of a plant GSNO reductase, suggesting that plants possess the enzymatic pathway that modulates the bioactivity and toxicity of NO.

At4g35050 showing homology to WD40 MSI3

Members of the MSI/RbAp sub-family of WD-repeat proteins are widespread in eukaryotic organisms and form part of multiprotein complexes that are involved in various biological pathways, including chromatin assembly, regulation of gene transcription, and cell division. The Zea mays RbAp-like protein (ZmRbAp1) binds acetylated histones H3 and H4 and suppresses mutations that have a negative effect on the Ras/cAMP pathway in yeast. The ZmRbAp genes form a gene family and are expressed in different tissues of Z. mays L. plants. Determination of its expression pattern during maize seed development revealed that ZmRbAp transcripts are abundant during the initial stages of endosperm formation. In addition, the transcripts are specifically localized in shoot apical meristem and leaf primordia of the embryo. ZmRbAp genes play a role in early endosperm differentiation and plant development (Rossi et al. (2001)). Also Rb proteins are known to be involved in multi-protein complexes; there are Rb binding protein characterized; and Rb plays a role in chromatin remodeling and cell cycle control and is important in development and growth of organs. The retinoblastoma (RB) protein regulates G1 progression and functions through its association with various cellular proteins. Two closely related mammalian RB binding proteins, RbAp48 and RbAp46, share sequence homology with the Msi1 protein of yeast. MSI1 is a multicopy suppressor of a mutation in the IRA1 gene involved in the Ras-cAMP pathway that regulates cellular growth. Human RbAp48 is present in protein complexes involved in histone acetylation and chromatin assembly. Four plant RbAp48- and Msi1-like proteins have been identified: one from tomato, LeMSI1, and three from Arabidopsis. LeMSI1 can function as a multicopy suppressor of the yeast ira1 mutant phenotype. The LeMSI1 protein localizes to the nucleus and binds to a 65-kD protein in wild-type as well as ripening inhibitor (rin) and Neverripe (Nr) tomato fruit. LeMSI1 also binds to the human RB protein and the RB-like RRB1 protein from maize, indicating that this interaction is conserved between plants and animals (Ach et al. (1997))

At4g36670 showing homology to Sugar transporter

The ERD6 clone is expressed after exposition to dehydration stress for 1 h. The ERD6 is related to those of sugar transporters of bacteria, yeasts, plants and mammals. Hydropathy analysis revealed that ERD6 protein has 12 putative transmembrane domains and a central hydrophilic region. Sequences that are conserved at the ends of the 6th and 12th membrane-spanning domains of sugar transporters are also present in ERD6. ERD6 gene is a member of a multigene family in the Arabidopsis genome. The expression of the ERD6 gene was induced not only by dehydration but also by cold treatment (Kiyosue et al. (1998)).

At5g01870 showing homology to Lipid transfer protein

Nonspecific lipid transfer proteins (LTPs) from plants are characterized by their ability to stimulate phospholipid transfer between membranes in vitro. However, because these proteins are generally located outside of the plasma membrane, it is unlikely that they have a similar role in vivo. The LTP1 promoter was active early in development in protoderm cells of embryos, vascular tissues, lignified tips of cotyledons, shoot meristem, and stipules. In adult plants, the gene was expressed in epidermal cells of young leaves and the stem. In flowers, expression was observed in the epidermis of all developing influorescence and flower organ primordia, the epidermis of the siliques and the outer ovule wall, the stigma, petal tips, and floral nectaries of mature flowers, and the petal/sepal abscission zone of mature siliques. Consistent with a role for the LTP1 gene product in some aspect of secretion or deposition of lipophilic substances in the cell walls of expanding epidermal cells and certain secretory tissues. The LTP1 promoter region contained sequences homologous to putative regulatory elements of genes in the phenylpropanoid biosynthetic pathway, suggesting that the expression of the LTP1 gene may be regulated by the same or similar mechanisms as genes in the phenylpropanoid pathway (Thoma, S. et al. (1994)). More background knowledge to this type of genes can be found in the following references: Clark, A. M. et al., (1999); Toonen, M. A. et al. (1997); Molina, A. (1997); Thoma, S. et al. (1994).

At5g02820 showing homology to SPO like

Plant steroid hormones, brassinosteroids (BRs), play important roles throughout plant growth and development. Plants defective in BR biosynthesis or perception display cell elongation defects and severe dwarfism. Two dwarf mutants named bin3 and bin5 with identical phenotypes to each other display some characteristics of BR mutants and are partially insensitive to exogenously applied BRs. In the dark, bin3 or bin5 seedlings are de-etiolated with short hypocotyls and open cotyledons. Light-grown mutant plants are dwarfs with short petioles, epinastic leaves, short inflorescence stems, and reduced apical dominance. We cloned BIN3 and BIN5 and show that BIN5 is one of three putative Arabidopsis SPO11 homologs (AtSPO11-3) that also shares significant homology to archaebacterial topoisomerase VI (TOP6) subunit A, whereas BIN3 represents a putative eukaryotic homolog of TOP6B. The pleiotropic dwarf phenotypes of bin5 establish that, unlike all of the other SPO11 homologs that are involved in meiosis, BIN5/AtSPO11-3 plays a major role during somatic development. Furthermore, microarray analysis of the expression of about 5500 genes in bin3 or bin5 mutants indicates that about 321 genes are down-regulated in both of the mutants, including 18 of 30 BR-induced genes. These results suggest that BIN3 and BIN5 may constitute an Arabidopsis topoisomerase VI that modulates expression of many genes,

including those regulated by BRs (Yin Y et al. (2002)). More background information on this type of genes can be found in the following references: Soustelle, C. et al. (2002); Kee, K. and Keeney, S. (2002); Hartung, F. and Puchta, H. (2001); Grelon, M. et al. (2001).

At5g14420 showing homology to copine I (phospholipid binding protein)

The copines are a newly identified class of calcium-dependent, phospholipid binding proteins that are present in a wide range of organisms, including Paramecium, plants, Caenorhabditis elegans, mouse, and human. However, the biological functions of the copines are unknown. It is described that a humidity-sensitive copine mutant was made in Arabidopsis and under nonpermissive, low-humidity conditions, the cpn1-1 mutant displayed aberrant regulation of cell death that included a lesion mimic phenotype and an accelerated hypersensitive response (HR). However, the HR in cpn1-1 showed no increase in sensitivity to low pathogen titers. Low-humidity-grown cpn1-1 mutants also exhibited morphological abnormalities, increased resistance to virulent strains of Pseudomonas syringae and Peronospora parasitica, and constitutive expression of pathogenesis-related (PR) genes. Growth of cpn1-1 under permissive, high-humidity conditions abolished the increased disease resistance, lesion mimic, and morphological mutant phenotypes but only partially alleviated the accelerated HR and constitutive PR gene expression phenotypes. The disease resistance phenotype of cpn1-1 suggests that the CPN1 gene regulates defense responses. Alternatively, the primary function ofCPN1 may be the regulation of plant responses to low humidity, and the effect of the cpn1-1 mutation on disease resistance may be indirect (Jambunathan et al. (2001)). Arabidopsis growth over a wide range of temperatures requires the BONZAI1 (BON1) gene because bon1 null mutants make miniature fertile plants at 22 degrees C but have wild-type appearance at 28 degrees C. The expression of BON1 and a BON1-associated protein (BAP1) is modulated by temperature. Thus BON1 and BAP1 may have a direct role in regulating cell expansion and cell division at lower temperatures. BON1 contains a Ca(2+)-dependent phospholipid-bindi.ng domain and is associated with the plasma membrane. It belongs to the copine gene family, which is conserved from protozoa to humans. Our data suggest that this gene family may function in the pathway of membrane trafficking in response to external conditions (Hua et al. (2001)). The major calcium-dependent, phospholipid-binding protein obtained from extracts of Paramecium tetraurelia, named copine, had a mass of 55 kDa, bound phosphatidylserine but not phosphatidylcholine at micromolar levels of calcium but not magnesium, and promoted lipid vesicle aggregation. Current sequence databases indicate the presence of multiple copine homologs in green plants, nematodes, and humans. The full-length sequences reveal that copines consist of two C2 domains at the N terminus followed by a domain similar to the A domain that mediates interactions between integrins and extracellular ligands. The association

with secretory vesicles, as well the general ability of copines to bind phospholipid bilayers in a calcium-dependent manner, suggests that these proteins may function in membrane trafficking (Creutz et al. (1998)).

At5g49160 showing homology to cytosine methyltransferase

DNMT3L is a regulator of imprint establishment of normally methylated maternal genomic sequences. DNMT3L shows high similarity to the de novo DNA methyltransferases, DNMT3A and DNMT3B, however, the amino acid residues needed for DNA cytosine methyltransferase activity have been lost from the DNMT3L protein sequence. Apart from methyltransferase activity, Dnmt3a and Dnmt3b serve as transcriptional repressors associating with histone deacetylase (HDAC) activity. DNMT3L can also repress transcription by binding directly to HDAC1 protein. PHD-like zinc finger of the ATRX domain is the main repression motif of DNMT3L, through which DNMT3L recruits the HDAC activity needed for transcriptional silencing. DNMT3L as a co-repressor protein and suggest that a transcriptionally repressed chromatin organisation through HDAC activity is needed for establishment of genomic imprints (Aapola et al. (2002)). More background information to this type of genes can be found in Chen, T. et al. (2002); Bartee, L. and Bender, J. (2001); Freitag M. et al. (2002). In Arabidopsis a SWI2/SNF2 chromatin remodeling factor-related protein DDM1 and a cytosine methyltransferase MET1 are required for maintenance of genomic cytosine methylation. Mutations in either gene cause global demethylation. There are also effects of these mutations on the PAI tryptophan biosynthetic gene family, which consists of four densely methylated genes arranged as a tail-to-tail inverted repeat plus two unlinked singlet genes. The methylation mutations caused only partial demethylation of the PAI loci: ddm1 had a strong effect on the singlet genes but a weaker effect on the inverted repeat, whereas met1 had a stronger effect on the inverted repeat than on the singlet genes. The double ddm1 met1 mutant also displayed partial demethylation of the PAI genes, with a pattern similar to the ddm1 single mutant. To determine the relationship between partial methylation and expression for the singlet PAI2 gene we constructed a novel reporter strain of Arabidopsis in which PAI2 silencing could be monitored by a blue fluorescent plant phenotype diagnostic of tryptophan pathway defects. This reporter strain revealed that intermediate levels of methylation correlate with intermediate suppression of the fluorescent phenotype. Other background information can be found in Finnegan, E. J. and Kovac K. A. (2000). Plant DNA methyltransferases. DNA methylation is an important modification of DNA that plays a role in genome management and in regulating gene expression during development. Methylation is carried out by DNA methyltransferases which catalyse the transfer of a methyl group to bases within the DNA helix. Plants have at least three classes of cytosine methyltransferase which differ in protein

structure and function. The METI family, homologues of the mouse Dnmtl methyltransferase, most likely function as maintenance methyltransferases, but may also play a role in de novo methylation. The chromomethylases, which are unique to plants, may preferentially methylate DNA in heterochromatin; the remaining class, with similarity to Dnmt3 methyltransferases of mammals, are putative de novo methyltransferases. The various classes of methyltransferase may show differential activity on cytosines in different sequence contexts. Chromomethylases may preferentially methylate cytosines in CpNpG sequences while the Arabidopsis METI methyltransferase shows a preference for cytosines in CpG sequences. Additional proteins, for example DDM1, a member of the SNF2/SWI2 family of chromatin remodelling proteins, are also required for methylation of plant DNA.

At5g54940 showing homology to Translation initiation factor (translational initiation factor eIF1),

Protein synthesis has not been considered to be fundamental in the control of cell proliferation. However, data are emerging on the involvement of this process in cell growth and tumorigenesis. Protein biosynthesis is a central process in all living cells. It is one of the last steps in the transmission of genetic information stored in DNA on the basis of which proteins are produced to maintain the specific biological function of a given cell. Protein synthesis takes place on ribosomal particles where the genetic information transcribed into mRNA is translated into protein. The process of protein synthesis on the ribosome consists of three phases: initiation, elongation and termination. Brassinosteroids (BRs) regulate the expression of numerous genes associated with plant development, and require the activity of a Ser/Thr receptor kinase to realize their effects. In animals, the transforming growth factor-beta (TGF-beta) family of peptides acts via Ser/Thr receptor kinases to have a major impact on several pathways involved in animal development and adult homeostasis. TGF-beta receptor-interacting protein (TRIP-1) was previously shown by others to be an intracellular substrate of the TGF-beta type II receptor kinase which plays an important role in TGF-beta signaling. TRIP-1 is a WD-repeat protein that also has a dual role as an essential subunit of the eukaryotic translation initiation factor eIF3 in animals, yeast and plants, thereby revealing a putative link between a developmental signaling pathway and the control of protein translation. In yeast, expression of a TRIP-1 homolog has also been closely associated with cell proliferation and progression through the cell cycle. We report here the novel observation that transcript levels of TRIP-1 homologs in plants are regulated by BR treatment under a variety of conditions, and that transgenic plants expressing antisense TRIP-1 RNA exhibit a broad range of developmental defects, including some that resemble the phenotype of BR-deficient and -insensitive mutants. This correlative evidence suggests that a WD-domain protein with

reported dual functions in vertebrates and fungi might mediate some of the molecular mechanisms underlying the regulation of plant growth and development by BRs (Jiang and Clouse (2001)). The Arabidopsis COP9 signalosome is a multisubunit repressor of photomorphogenesis that is conserved among eukaryotes. This complex may have a general role in development. association between components of the COP9 signalosome (CSN1, CSN7, and CSN8) and two subunits of eukaryotic translation initiation factor 3 (eIF3), eIF3e (p48, known also as INT-6) and eIF3c (p105). AteIF3e coimmunoprecipitated with CSN7, and eIF3c coimmunoprecipitated with eIF3e, eIF3b, CSN8, and CSN1. eIF3e directly interacted with CSN7 and eIF3c. eIF3e and eIF3c are probably components of multiple complexes and that eIF3e and eIF3c associate with subunits of the COP9 signalosome, even though they are not components of the COP9 signalosome core complex. This interaction may allow for translational control by the COP9 signalosome (Yahalom et al. (2001)).

At5g56740 showing homology to Histone acethyl transferase HATB

Transforming viral proteins such as E1A which force quiescent cells into S phase have two essential cellular target proteins, Rb and CBP/p300. Rb regulates the G1/S transition by controlling the transcription factor E2F. CBP/p300 is a transcriptional co-activator with intrinsic histone acetyl-transferase activity. This activity is regulated in a cell cycle dependent manner and shows a peak at the G1/S transition. CBP/p300 is essential for the activity of E2F, a transcription factor that controls the G1/S transition. In addition, our results suggest that CBP HAT activity is required both for the G1/S transition and for E2F activity. Thus CBP/p300 seems to be a versatile protein involved in opposing cellular processes, which raises the question of how its multiple activities are regulated (Ait-Si-Ali, S. et al (2000)). The BRCA2 is a histone acetyltransferase.Two potential functions of BRCA2 were proposed which includes role in the regulation of transcription and also in DNA repair. Forty-five-amino acid region encoded by exon 3 of BRCA2 was shown to have transcriptional activation function. Recent studies of the several enzymes involved in acetylation and deacetylation of histone residues have revealed a possible relationship between gene transcriptional activation and histone acetylation. Since BRCA2 appear to function as a transcriptional factor, we have tested for Histone acetyl transferase (HAT) activity of BRCA2. Here, we present evidence that BRCA2 hasintrinsic HAT activity, which maps to the amino-terminal region of BRCA2. Our results demonstrate that BRCA2 proteins acetylate primarily H3 and H4 of free histones. These observations suggest that HAT activity of BRCA2 may play an importantrole in the regulation of transcription and tumor suppressor function (Siddique et al. (1998)). These type of genes are very important for regulation of genes involved in development, cell cycle control, chromatin structure.

At5g61520 showing homology to STP3 sucrose transporter

For developing seeds of grain legumes, photoassimilates released to the seed apoplasm from maternal seed coats are retrieved by abaxial epidermal and subepidermal cells (dermal cell complexes) of cotyledons followed by symplasmic passage to their underlying storage parenchyma cells. In some species, the cells of these complexes differentiate into transfer cells (e.g. broad bean and pea, Patrick and Offler,2001). Sucrose is a major component of the photoassimilates delivered to the cotyledons (Patrick and Offler, 2001; Weber et al., 1997b). Sucrose transporter (SUT) genes have been cloned, and functionally characterised as sucrose/H+ symporters, from developing cotyledons of broad bean (VfSUT1, Weber et al., 1997a) and pea (PsSUT1, Tegeder et al., 1999). SUTs and P-type H+-ATPases have been shown to co-localise to plasma membranes of dermal cell complexes in developing cotyledons of broad bean (Harrington et al., 1997; Weber et al., 1997a) and French bean (Tegeder et al., 2000). In contrast, for pea cotyledons, SUT is also present in storage parenchyma cells, but is 4-fold less active than SUT(s) localised to epidermal transfer cells (Tegeder et al., 1999). These type of genes are Important for seed filling.

At5g66210 showing homology to Calcium dependent protein kinase

In plants, numerous Ca(2+)-stimulated protein kinase activities occur through calcium-dependent protein kinases (CDPKs). These novel calcium sensors are likely to be crucial mediators of responses to diverse endogenous and environmental cues. However, the precise biological function(s) of most CDPKs remains elusive. The Arabidopsis genome is predicted to encode 34 different CDPKs. In this Update, we analyze the Arabidopsis CDPK gene family and review the expression, regulation, and possible functions of plant CDPKs. By combining emerging cellular and genomic technologies with genetic and biochemical approaches, the characterization of Arabidopsis CDPKs provides a valuable opportunity to understand the plant calcium-signaling network (Cheng et al., 2002). These type of genes are Important for stress signaling.

At2g25970 showing homology to KH RNA binding domain

Lorkovic and Barta described RNA recognition motif (RRM) and K homology (KH) domain RNA-binding proteins from the flowering plant Arabidopsis thaliana (2002). The most widely spread motifs are the RNA recognition motif (RRM) and the K homology (KH) domain. The Arabidopsis genome encodes 196 RRM-containing proteins, a more complex set than found in Caenorhabditis elegans and Drosophila melanogaster. In addition, the Arabidopsis genome

contains 26 KH domain proteins. Most of the Arabidopsis RRM-containing proteins can be classified into structural and/or functional groups, based on similarity with either known metazoan or Arabidopsis proteins. Approximately 50% of Arabidopsis RRM-containing proteins do not have obvious homologues in metazoa, and for most of those that are predicted to be orthologues of metazoan proteins, no experimental data exist to confirm this. Additionally, the function of most Arabidopsis RRM proteins and of all KH proteins is unknown. The higher complexity of RNA-binding proteins in Arabidopsis, as evident in groups of SR splicing factors and poly(A)-binding proteins, may account for the observed differences in mRNA maturation between plants and metazoa. The function of this type of genes is largely unknown, but could be related to PUMILIO genes from drosophila. Important for regulation of gene expression at the post-transcriptional level, role in development, stress tolerance.

At3g07800 showing homology to Thymidine kinase

This type of genes is cell cycle regulated, E2F regulated, is responsible for production of thymidine triphosphate. This type of gene plays a role as a precursor for DNA synthesis and is therefore a marker of S phase.

At5g47370 showing homology to Homeobox leucine zipper protein

This type of genes is important for development and growth and also for stress tolerance.

Example 7: Rice transformation with the genes according to the present invention

In a particular example of the present invention, the genes as identified above are cloned into a plant expression vector operably linked to suitable regulatory elements to drive overexpression or downregulation of these genes. These vectors are subsequently transferred to the rice plant according to the following protocol.

Mature dry seeds of the rice japonica cultivar Taipei were dehusked. Sterilization was carried out by incubating for one minute in 70% ethanol, followed by 30 minutes in 0.2%HgCl2, followed by a 6 times 15 minutes wash with sterile distilled water. The sterile seeds were then germinated on a medium containing 2,4-D (callus induction medium). After incubation in the dark for four weeks, embryogenic, scutellum-derived calli were excised and propagated on the same medium. After two weeks the calli were multiplied or propagated by subculture on the same medium for another 2 weeks. Embryogenic callus pieces were sub-cultured on fresh medium 3 days before co-cultivation (to boost cell division activity). Agrobacterium strain LBA4404 harboring binary T-DNA vectors were used for cocultivation. Agrobacterium was inoculated on AB medium with the appropriate antibiotics and cultured for 3 days at 28°C. The

bacteria were then collected and suspended in liquid co-cultivation medium to a density (OD600) of about 1. The suspension was then transferred to a petri dish and the calli immersed in the suspension for 15 minutes. The callus tissues were then blotted dry on a filter paper and transferred to solidified, co-cultivation medium and incubated for 3 days in the dark at 25°C. Co-cultivated calli were grown on 2,4-D-containing medium for 4 weeks in the dark at 28°C in the presence of a suitable concentration of the selective agent. During this period, rapidly growing resistant callus islands developed. After transfer of this material to a regeneration medium and incubation in the light, the embryogenic potential was released and shoots developed in the next four to five weeks. Shoots were excised from the calli and incubated for 2 to 3 weeks on an auxin-containing medium from which they were transferred to soil. Hardened shoots were grown under high humidity and short days in a greenhouse. Seeds were then harvested three to five months after transplanting. The method yielded single locus transformants at a rate of over 50 % (Aldemita and Hodges1996, Chan et al. (1993), Hiei et al. (1994)).

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Table 1. Arabidopsis Genes 2-fold or more upregulated in E2Fa/DPa plants							
Gene Identification	**accession #**	**MIPS name**	**SEQ ID NO**	**SEQ ID NO**	**Fold induction**	**E2F site**	**Plant homologue**
Unknown function (14)			cDNA	PROTEIN			
hypothetical protein	AI998042	At1g57680	1	53	2.66		rice BAB90159.1, maize AY107220.1
putative protein	AI994686	At3g45730	2	54	5.14		
putative protein	AI994734	At5g66580	4	56	3.18		
unknown protein	AI999397	At2g38310	5	57	2.79	TTTGCCCC	rice BAB68102.1
unknown protein	AI995465	At2g47440	7	59	2.50		
unknown protein	AI994871	At1g76970	8	60	2.34		rice BAB78689.1, corn AAB00079.1
hypothetical protein, kinesin	AI998366	At1g27500	9	61	2.21		rice AAL87057.1
putative protein	AI996967	At4g33050	10	62	2.20		rice BAB90008.1
putative protein	AI995917	At3g43690	12	64	2.18		
unknown protein, kh domain protein	AI993084	At2g25970	13	65	2.15		rice BAA92910.1, maize AY106526.1
unknown protein	AI993077	At1g68580	14	66	2.13		rice BAC00723.1, corn AAK11516.1
putative protein, copine	AI993019	At5g14420	15	67	2.05		rice BAB92575.1
hypothetical protein	AI997428	At1g57990	16	68	2.02		rice BAB90042.1
unknown protein	AI997827	At5g53740	17	69	2.01		
DNA replication and modification (14)							
putative thymidine kinase	AI997851	At3g07800			8.44		rice AAC31168.1
DNA methyltransferase	AI994691	At5g49160			5.37	ATTGCCGC	rice AAL77415.1, corn AAC16389.1
Msi3	AW004204	At4g35050			4.89	TTTCCCGC	corn AAL33648.1
putative linker histone protein	AI994590	At3g18035			3.31		
putative replication factor c	AI997934	At1g21690			3.30	TTTCCCGC	
topoisomerase 6 subunit A	AI995290	At5g02820			2.62	TTTCCCGC	
histone H4-like protein	AI999171	At3g46320			2.55	TTTGGCGC	
histone acetylase HAT B	AI998229	At5g56740			2.36	TTTCCCGC	corn AAM28228.1
putative histon H1	AI996137	At1g06760			2.27		
histone H2A-like protein	AI995882	At4g27230			2.23		
putative DNA gyrase subunit A	AI995400	At3g10690			2.20		rice AAD29710.1
histone H2B-like protein	AI999101	At5g59910			2.16		
putative mismatch binding protein	AI993280	At3g24320			2.10		rice CAD41187.1, corn AAF35250.1
adenosylhomocysteinase	AI996953	At4g13940			2.07		corn AAL33588.1
Cell Cycle (2)							
E2Fa	AJ294534	At2g36010			94.88		
CDKB1;1	D10851	At3g54180			2.60	TTTCCCG	

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Cell wall biogenesis (11)							
xyloglucan endo-1,4-beta-D-glucanase (meri-5)	AI994459	At4g30270			3.74		
putative glycosyl transferase	AI999244	At1g70090			3.38		
alpha galactosyltransferase-like protein	AI998223	At3g62720			3.26		
putative xyloglucan endotransglycosylase	AI999683	At3g23730			2.85		rice CAD41426.1, corn CAB510059.1
xyloglucan endo-1,4-beta-D-glucanase-like protein	AI998301	At4g30280			2.74		
putative xyloglucan endotransglycosylase	AI994477	At1g14720			2.51		
putative glycosyl transferase	AI999770	At1g24170			2.39		
putative UDP-glucose glucosyltransferase	AI997288	At1g22400			2.34	TTTCCCG C	
putative glucosyltransferase	AI998872	At2g15480			2.15		
peroxidase	AI994622	At2g38380			2.11	TTTCGCC C	
beta-1,3-glucanase-like protein	AI994681	At3g55430			2.05		rice AAB37697.1, corn CAB96424.1
Chloroplastic genes (7)							
large subunit of ribulose-1,5-bisphosphate carboxylase/oxygenase	N96785	rbcL			4.71		
ribosomal protein L33	AI994194	rpl33			3.54		
PSII I protein	AW004203	psbI			2.81		
ribosomal protein L2	AW004266	rpl2			2.61		
ATP-dependent protease subunit	AI997947	clpP			2.60		
cytochrome B6	AI997102	petB			2.55		
ATPase epsilon subunit	AW004251	atpE			2.17		
Mitochondrial genes (1)							
26S ribosomal RNA protein	AW004275	orf107a			2.87		
Transcription factors (6)							
LOB domain protien 41	AI996685	At3g02550	3	55	4.01		riceBAB92193.1
WRKY transcription factor 21	AI992739	At2g30590			2.78	TTTCCCC C	
GATA Zn-finger protein	AI995731	At3g16870	6	58	2.75		maize AY072149
Anthocyaninless2	AI993655	At4g00730			2.73	TTTCCCC C	
leucine zipper-containing protein	AI995691	At1g07000			2.43		
homeodomain transcription factor (Athb-6)	AI999190	At2g22430			2.30		rice CAA65456.2, corn CAB96424.1
Metabolism and blogenesis (11)							
alcohol dehydrogenase	AI998773	At1g77120			5.09		
putative isocistrate lyase	AI999168	At3g21720			3.08		
protochlorophyllide reductase precursor	AI993342	At4g27440			2.39		
suger transpoter like protein	AI997793	At4g36670			2.27		rice AAK13147.1, corn AAF74568.1

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NADH-dependent glutamate synthase (GOGAT)	AI997600	At5g53460			2.25		
nitrate reductase (NIA2)	AI996208	At1g37130			2.15		
pectate lyase - like protein	AJ508995	At3g54920			2.13		
putative sterol dehydrogenase	AI996340	At2g43420			2.10		
glutamine synthetase root isozyme 1 (GS)	161G19T7	At1g66200			2.06		
monosaccharide transporter STP3	AI997045	At5g61520			2.05		rice BAA83554.1, corn AAF74568.1
Signal transduction (6)							
calcium-dependent protein kinase	AI996555	At5g66210			2.96		rice AAF23901.2, corn BAA12715.1
WD-40 repeat protein	AI993055	At5g14530			2.70		rice AD27557.1, corn AAA50446.1
receptor-protien kinase-like protein	AI994727	At5g54380			2.59		rice AAK63934.1, corn AAB09771.1
putative phytochrome A	AI998146	At1g09570			2.45		
putative leucine-rich receptor-like protein kinase	AI999651	At1g72180			2.13		rice BAC06203.1, corn CAC35411.1
putative receptor-like kinase	AI993298	At3g23750			2.06		rice CAA69028.1, corn CAC35412.1
Others (13)							
putative pollen allergen	AI996548	At3g45970			3.22		rice AAG13596.1, corn CAD40849.1
cold-regulated protein COR6,6	AW004198	At5g15970			3.03		
phi-1-like protein	AI994601	At5g64260			2.60		
lipid-transfer protein-like	AI998609	At5g01870			2.33		rice BAB86497.1, corn AAB06443.1
DnaJ homologue	AI994551	At5g06910			2.32	ATTGGCGC	
blue copper binding protein	AI996535	At5g20230			2.30		
src-2 like protein	AI998679	At1g09070	11	63	2.19		
RING finger protein	AI999491	At3g61460			2.14		rice BAA85438.1, corn AAL59234.1
putative Ticc22	AI993361	At3g23710			2.14		
nodulin-like protein	AI996322	At1g80530			2.07		rice AAM01022.1
putative resistance protein	AI997549	At1g61100			2.06		rice AAL83695.1,
seed imbitition protein-like	AI993446	At5g20250			2.05		
putative disease resistance protein	AI998978	At1g72900			2.04		rice AAL01163.1, corn AAC83564.1

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Table 2. Arabidopsis Genes 2-fold or more repressed in E2Fa/DPa plants

Gene Identification	accession #	MIPS	SEQ ID NO	SEQ ID NO	Fold repression	E2F site	plant homologue
Unknown function (35)							
unknown protein	AI993767	At1g45200 *	18	70	3.91		
putative protein	AI993468	At3g56290	19	71	3.38		maize AY106321.1 , rice BAB93184.1
hypothetical protein, multidrug efflux protein	AI996374	At1g61890	21	73	2.78		
unknown protein	AI994573	At3g15950	22	74	2.71		
putative protein	AI994726	At3g52360	23	75	2.65		
hypothetical protein	AI997393	At4g02920	24	76	2.60	TTTGCCCC	Y09602. Hordeum vulgare
unknown protein, put protease inhibitor	AJ508997	At5g43580	25	77	2.58		
unknown protein	AI997866	At1g70760	26	78	2.52		
unknown protein	AI997085	At5g43750	27	79	2.51		rice BAB90754.1
putative protein	AI995724	At5g50100 **	28	80	2.48		rice AL606619.2 OSJN00032 genomic
unknown protein	AI995337	At1g74880	29	81	2.42		maize AY105515.1, rice BAB89011.1
unknown protein	AI998296	At3g19370	30	82	2.40		
unknown protein, ATP ase	AI993346	At3g10420	31	83	2.40		
putative protein	AI999485	At3g61080	32	84	2.38		
unknown protein	AI996923	At1g67860	33	85	2.38		
unknown protein	AI994841	At1g52870	34	86	2.35	ATTCCCCC	maize AY108423.1
unknown protein	AI999581	At1g64370	35	87	2.35		
unknown protein	AI997584	At1g05870	36	88	2.25		rice BAB86085.1, maize Y110580.1
putative protein	AI992938	At5g03540	37	89	2.21		
hypothetical protein	AI997712	At2g15020	38	90	2.21		rice BAB64794.1
unknown protein	AI998338	At1g68440	39	91	2.20		
unknown protein	AI996872	At2g21960	40	92	2.19		
putative protein, centrin	AI996295	At4g27280	41	93	2.18		
putative protein	AI995642	At3g48200	42	94	2.16		
unknown protein	AI997470	At2g32870	43	95	2.14		
hypothetical protein	AI998460	At1g69510	44	96	2.11	TTTGGCCC	rice BAB18340.1, maize AY110240.1
putative triacylglycerol lipase	AI993356	At5g22460	45	97	2.10		
putative protein	AI995956	At5g52060	46	98	2.08		
unknown protein	AI996100	At2g35830	47	99	2.06		
hypothetical protein	AI996039	At3g27050	48	100	2.05		
unknown protein	AI996020	At5g51720	49	101	2.04		
putative protein	AW004101	At4g39730	51	103	2.03		
hypothetical protein	AI998372	At2g01260	52	104	2.03		
unknown protein	AI999573	At3g61060			2.00		
unknown protein	AI998562	At2g35760			2.00		

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No hit (2)								
no hit on genome	AI995690				2.54			
no hit on genome	AI999010				2.23			
Cell wall biogenesis (4)								
similar to polygalacturonase-like protein	AI993509	At1g10640	50	102	3.62		maize AY106712.1, rice BAC06884.1	
putative xyloglucan endo-transglycosylase	AI997647	At2g36870			2.51			
pectate lyase 1-like protein	AI994801	At1g67750			2.40			
xyloglucan endo-transglycosylase	AI998832	At3g44990			2.35			
Metabolism and biogenesis (24)								
fructose-biphosphate aldolase-like protein	AI994456	At4g26530			5.99	ATTGGCCC		
sucrose-phosphate synthase-like protein	AI995432	At4g10120			4.64			
putative branched-chain amino acid aminotransferase	AI997263	At3g19710			3.31			
vitamine c-2	AI997404	At4g26850	20	72	3.04	TTTGCCGC	maize AY105327, rice BAB90526.1	
nicotianamine synthase	AI993200	At5g04950			2.86			
beta-fructosidase	AI994670	At1g62660			2.66	TTTCCCCC		
neoxanthin cleavage enzyme-like protein	AI997269	At4g19170			2.66			
putative starch synthase	AI997174	At1g32900			2.63			
cytochrome P450 monooxygenase (CYP83A1)	AI994017	At4g13770			2.57			
beta-amylase-like protein	AI999322	At5g18670			2.53			
FRO1-like protein; NADPH oxidase-like	AI995987	At5g49740			2.46			
putative hydrolase	AI997149	At3g48420			2.39			
furamate hydratase	AI997067	At5g50950			2.31	TTTGGCCC		
5'-adenylylsulfate reductase	AI992757	At1g62180			2.30	TTTCCCCC		
5'-adenylylsulfate reductase	AI996614	At4g04610			2.30			
UDP rhamnose-anthocyanidin-3-glucoside rhamnosyltransferase - like protein	AI996803	At4g27560			2.24			
cytochrome P450-like protein	AI993171	At5g48000			2.23			
lactoylglutathione lyase-like protein	AI994552	At1g11840			2.20			
putative beta-glucosidase	AI995306	At4g27820			2.20	ATTGGCCC		
adenine phosphoribosyltransferase-like protein	AI994567	At4g22570			2.18			
catalase	AI995830	At4g35090			2.17	ATTCCCCC		
putative glutathione peroxidase	AW004143	At2g25080			2.15			

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putative adenosine phosphosulfate kinase	AW004219	At2g14750			2.13			
tyrosine transaminase like protein	AI996914	At4g23600			2.13			
Transcription factors (5)								
homeobox-leucine zipper protein ATHB-12	AI994027	At3g61890			4.20			
NAC domain protein NAC2	AI992865	At1g69490			3.68			
myb-related transcription factor	AI995298	At1g71030			2.78			
dof zinc finger protein	AI994875	At1g51700			2.30			
MYB-related transcription factor (CCA1)	AI992931	At2g46830			2.19			
Signal transduction (9)								
serine/threonine protein kinase-like protein	AI995557	At5g10930			3.91			
subtilisin proteinase-like	AI993428	At4g21650			3.19			
putative oligopeptide transporter	AI996160	At4g10770			2.68			
putative lectin	AI998542	At3g16400			2.52			
Ca2+dependent membrane-binding protein annexin	AI998553	At1g35720			2.45			
putative WD repeat protein	AI997238	At3g15880			2.38			
putative lectin	AI999016	At3g16390			2.35			
putative lectin	AI993358	At3g16530			2.31			
SNF1 related protein kinase (ATSRPK1)	AI993111	At3g23000			2.06			
Others (25)								
putative protease inhibitor Dr4	AI995265	At1g73330			10.30			
major latex protein homolog - like	AI998305	At2g01520			4.27			
pollen allergen-like protein	AI993041	At1g24020			3.56			
putative heat shock protein	AI997846	At1g06460			3.55			
putative fibrillin	AI997199	At4g04020			3.55			
major latex protein homolog - like	AI997255	At1g70890			3.50			
putative nematode-resistance protein	AI993740	At2g40000			2.95			
putative auxin-regulated protein	AJ508998	At2g46690			2.86			
putative myrosinase-binding protein	AI997583	At2g39310			2.61			
ubiquitin-conjugating enzyme-like protein	AI997782	At5g56150			2.41			
ubiquitin-conjugating enzyme E2-17 kD 8	AI994771	At5g41700			2.40			
vegetative storage protein Vsp2	AI999152	At5g24770			2.35			
heat shock protein 70	AI994044	At3g12580			2.24			
chloroplast outer envelope membrane	AI997015	At3g63160			2.20			

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protein								
translation initiation factor-like protein	AI992786	At5g54940			2.15			
pseudogene	AI995323	At2g04110			2.07			
vegetative storage protein Vsp1	AI999546	At5g24780			2.06			
dehydrin ERD10	AI997518	At1g20450			2.06			
MTN3-like protein	AI997159	At3g48740			2.05			
putative chlorophyll A-B binding protein	AI994859	At3g27690			2.05			
photosystem I reaction centre subunit psaN	AI997939	At5g64040			2.03			
AR781, similar to yeast pheromone receptor	AI998194	At2g26530			2.03			
putative lipid transfer protein	AI997024	At2g15050			2.03			
peroxidase ATP3a	AI998372	At5g64100			2.03			
myosin heavy chain-like protein	AI999224	At3g16000			2.01			

- * this sequence is present in the MIPs database version of 25 july 2002
- ** this record has a n updates MIPS accession number At5g50101.

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Table 3. Number of E2F elements in the different datasets			
	All genes (4518)	Upregulated genes (88)	Downregulated genes (105)
TTTCCCCC	62	2	3
TTTCCCGC	40	6	0
TTTCGCCC	15	0	0
TTTCGCCC	13	1	0
TTTGCCCC	37	1	1
TTTGCCGC	20	0	1
TTTGGCCC	55	0	2
TTTGGCGC	15	1	0
ATTCCCCC	10	0	2
ATTCCCGC	6	0	0
ATTCGCCC	8	0	0
ATTCGCCC	14	0	0
ATTGCCCC	13	0	0
ATTGCCGC	10	1	0
ATTGGCCC	44	0	2
ATTGGCGC	9	1	0
Total	371	13	11

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	Tab 4: Arabidopsis genes 1.3 fold or more upregulated in E2Fa/Dpa plants			
	Gene name	e_value	MIPS accession number	ratio
1	putative protein	0	At5g51100	1.42
2	endo-1,4-beta-glucanase	9E-27	At1g70710	1.85
3	mitochondrial elongation factor Tu	1E-125	At4g02930	1.39
4	glycine-rich protein (clone AtGRP8)	1E-155	At4g39260	1.33
5	UTP-glucose glucosyltransferase	0	At5g66690	1.59
6	lipid-transfer protein-like	0	At5g01870	2.33
7	putative auxin-regulated protein	6E-68	At4g34760	1.48
8	histone H1, putative	0	At1g06760	2.27
9	APETALA2 protein	0	At4g36920	1.44
10	putative histone H2A	0	At1g08880	1.84
11	monosaccharide transporter STP3	2E-69	At5g61520	2.05
12	receptor-protein kinase-like protein	8E-64	At3g51550	1.33
13	SET-domain protein-like	1E-140	At5g04940	1.38
14	homeodomain transcription factor (ATHB-6)	0	At2g22430	2.30
15	putative protein	0	At4g33700	1.85
16	hypothetical protein	1E-139	At1g05800	1.34
17	unknown protein	0	At1g33410	1.37
18	hypothetical protein	1E-140	At4g17060	1.41
19	putative protein	0	At5g19820	1.44
20	putative protein	1E-16	At3g53670	1.54
21	regulatory subunit of protein kinase CK2	0	At3g60250	1.51
22	delta 9 desaturase, putative	0	At1g06090	1.85
23	putative protein	0	At5g06360	1.48
24	acetyl-CoA carboxylase, putative, 5' partial	0	At1g36170	1.49
25	hypothetical protein	0	At1g56150	1.97
26	seed imbitition protein-like	0	At5g20250	2.05
27	unknown protein	1E-146	At1g76010	1.64
28	homeobox-leucine zipper protein-like	0	At5g47370	2.21
29	kinesin-like protein	0	At5g54670	1.69
30	putative protein	0	At3g48050	1.75
31	putative protein	0	At5g03040	1.34
32	xyloglucan endo-1,4-beta-D-glucanase precursor	0	At4g30270	3.74
33	putative WD-40 repeat protein	0	At2g19540	1.75
34	putative protein	1E-132	At3g54480	1.44
35	hypothetical protein	0	At1g15750	1.70
36	hypothetical protein	0	At1g66200	2.06
37	putative protein	0	At3g50630	1.40
38	unknown protein	0	At2g30930	1.30
39	putative protein	6E-91	At5g37720	1.80
40	unknown protein	1E-146	At5g54310	1.61
41	hypothetical protein	0	At1g48920	1.98
42	hypothetical protein	0	At1g17750	1.38
43	nuclear RNA binding protein A-like protein	0	At4g17520	1.43
44	unknown protein	0.0004	At1g10890	1.38
45	histone H2A- like protein	0	At4g27230	2.23

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46	phytochelatin synthase (gb|AAD41794.1)	0	At5g44070	1.39
47	RNA-binding protein cp29 protein	1E-159	At3g53460	1.54
48	putative RNA-binding protein	0	At3g25150	1.48
49	alcohol dehydrogenase	0.2	At5g42250	1.34
50	putative 60S ribosomal protein L6	1E-170	At1g74060	1.37
51	calmodulin-binding protein	1E-114	At5g57580	1.40
52	putative protein	3E-23	At4g20310	2.01
53	putative protein kinase	0	At1g08720	1.33
54	hypothetical protein	0	At3g12200	1.34
55	putative phosphatidylserine decarboxylase	0	At4g25970	1.38
56	unknown protein	0	At2g03120	1.31
57	unknown protein	0	At1g14880	1.48
58	histone H2A.F/Z	0	At3g54560	1.85
59	4-coumarate-CoA ligase - like	0	At4g19010	1.35
60	putative protein	0	At3g45040	1.72
61	unknown protein	0	At3g19540	1.84
62	putative protein	0	At4g34410	1.36
63		0	At1g61260	1.97
64	putative protein	0	At3g61490	1.32
65	lipoxygenase	0	At1g17420	1.34
66	putative SecA-type chloroplast protein transport factor	0	At4g01800	1.38
67	putative DNA-binding protein	0	At4g01250	1.49
68	hypothetical protein	0	At1g20580	1.37
69	hypothetical protein	2E-90	At1g47530	1.39
70	unknown protein	0	At2g37570	1.84
71	bZIP transcription factor-like protein	0	At3g62420	1.32
72	putative protein	1E-154	At3g56720	1.39
73	hypothetical protein	0	At1g76860	1.32
74	6-phosphogluconate dehydrogenase	2E-80	At5g41670	1.48
75	ferritin 1 precursor	0	At5g01600	1.38
76	putative ABC transporter	0	At1g71330	1.71
77	hypothetical protein	0	At1g27300	1.30
78	myrosinase precursor	0.87	At5g26000	2.81
79	unknown protein	0	At1g10270	1.47
80	putative protein	3E-88	At5g18650	1.33
81	hypothetical protein	6E-40	At2g36090	1.32
82	unknown protein	0	At1g43910	1.42
83	hypothetical protein	0	At1g07000	2.43
84	hypothetical protein	0	At1g18260	1.43
85	putative pre-mRNA splicing factor	0	At4g03430	1.49
86	putative protein	0	At5g11810	1.32
87	hypothetical protein	1E-151	At4g30150	1.41
88	S-receptor kinase -like protein	0	At4g32300	1.52
89	disease resistance RPP5 like protein	1E-175	At4g16950	1.64
90	unknown protein	2E-58	At1g76520	1.44
91	putative protein	1E-144	At5g14420	2.05
92	putative glucosyltransferase	4E-78	At1g23480	1.31
93	putative protein	1E-144	At4g28470	1.34

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94	putative protein	0	At4g29830	1.55
95	putative auxin-regulated protein	0	At2g33830	1.41
96	putative protein	7.9	At5g61550	1.38
97	unknown protein	0	At1g44810	1.39
98	protein phosphatase - like protein	1E-59	At5g02760	1.76
99	hypothetical protein	2E-21	At4g17800	1.59
100	hypothetical protein	0	At1g54080	1.58
101	xyloglucan endo-transglycosylase, putative	0	At1g14720	2.51
102	putative protein	0	At3g49320	1.70
103	beta-1,3-glucanase - like protein	0	At3g55430	2.05
104	putative protein	0	At3g45730	5.14
105	ubiquitin-conjugating enzyme E2-21 kD 1 (ubiquitin-protein ligase	0	At5g41340	1.32
106	putative reticuline oxidase-like protein	0	At1g30720	1.31
107	DNA (cytosine-5)-methyltransferase (DNA methyltransferase) (DNA	0	At5g49160	5.37
108	putative protein	0	At4g32030	1.38
109	unknown protein	0.000000003	At2g32710	1.46
110	E2F transcription factor-1 E2F1	1E-155	At5g22220	1.52
111	putative protein	0	At5g48820	1.80
112	putative E2F5 family transcription factor	1E-154	At2g36010	94.88
113				1.48
114	protein kinase cdc2 homolog B	0	At3g54180	2.60
115	putative WRKY DNA-binding protein	1E-164	At2g03340	1.43
116	hypothetical protein	0	At4g13670	1.56
117	xyloglucan endo-1,4-beta-D-glucanase-like protein	0	At4g30280	2.74
118	hypothetical protein	1E-121	At1g18630	1.41
119	putative protein	0	At5g35735	1.52
120	putative protein kinase	0	At2g47060	1.32
121	putative protein	0.1	At3g43690	2.18
122	70kD heat shock protein	0	At2g32120	1.57
123	nitrate reductase	0	At1g37130	2.15
124	beta-amylase	0	At5g55700	1.55
125	multicatalytic endopeptidase complex alpha chain	0	At3g51260	1.57
126	putative protein	0.029	At5g36190	2.55
127	putative protein	0	At4g00830	1.39
128	monodehydroascorbate reductase (NADH) - like protein	0	At5g03630	1.33
129	unknown protein	1E-107	At3g04350	1.42
130	hypothetical protein	0	At1g70090	3.38
131	E2 ubiquitin-conjugating-like enzyme Ahus5	0	At3g57870	1.38
132	putative protein	5E-25	At3g63070	1.35
133	hypothetical protein	0	At4g28330	2.23
134	cellulose synthase catalytic subunit, putative	1E-174	At1g55850	2.07
135	putative protein	0	At5g46410	1.54
136	putative polynucleotide phosphorylase	1E-136	At3g03710	1.53
137	hypothetical protein	0	At1g19180	1.32
138	hypothetical protein	0	At3g12270	1.83
139	sugar transporter like protein	0	At4g36670	2.27
140	hypothetical protein	1E-105	At2g39910	1.30

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141	putative phytochrome A	0	At1g09570	2.45
142	hypothetical protein	0	At1g64600	1.49
143	putative protein	0	At5g23610	1.60
144	putative protein	1E-177	At3g56360	1.39
145	cyclophylin -like protein	0	At3g63400	1.33
146	unknown protein	0	At2g37940	1.35
147	zinc finger protein, putative	1E-53	At1g75540	1.46
148	putative protein kinase	1E-19	At2g24360	1.48
149	putative glucosyltransferase	0	At2g15490	2.15
150		0	At1g60140	1.72
151	unknown protein	0	At1g43850	1.45
152	hypothetical protein	0	At3g14120	1.77
153	putative AP2 domain transcription factor	0	At2g41710	1.65
154	transcriptional regulator protein, putative	6E-71	At3g26640	1.51
155	hypothetical protein	0.026	At1g55370	1.35
156	unknown protein	0	At3g28920	1.93
157	hypothetical protein	0	At3g03750	1.43
158	hypothetical protein	2E-12	At4g27610	1.34
159	translation initiation factor eIF-2 beta chain - like protein	2E-11	At5g20920	1.33
160	unknown protein	0	At2g26280	1.53
161	unknown protein; similar to ESTs gb|T41672.1, gb|AI992710.1, and	0	At1g78420	1.39
162	elongation factor, putative	3E-14	At1g56070	1.99
163	anthranilate N-benzoyltransferase - like protein	1E-120	At5g01210	1.66
164	putative protein	1E-178	At4g39680	1.43
165	unknown protein	0	At3g05380	1.92
166	splicing factor At-SRp40	0	At4g25500	1.52
167	cdc2-like protein kinase	0	At5g10270	1.77
168	calcium-dependent protein kinase	1E-169	At3g57530	1.39
169	phosphoprotein phosphatase, type 1 catalytic subunit	0	At2g29400	1.48
170	putative mitochondrial translation elongation factor G	0	At2g45030	1.65
171	long-chain-fatty-acid--CoA ligase-like protein	0	At5g27600	1.34
172	cytochrome c, putative	4E-26	At3g27240	1.36
173	En/Spm-like transposon protein	0	At2g40070	1.41
174	putative phospho-ser/thr phosphatase	0	At4g03080	1.41
175	chloroplast 50S ribosomal protein L22, putative	6E-77	At1g52370	1.40
176	unknown protein	0	At2g15890	1.34
177	putative protein	0	At4g26750	1.55
178	receptor-protein kinase-like protein	0	At5g54380	2.59
179				1.55
180	phosphoglycerate kinase, putative	1E-155	At3g12780	1.88
181	putative HMG protein	0	At2g17560	1.45
182	hypothetical protein	0	At1g76100	1.36
183	protein kinase cdc2 homolog B	0	At3g54180	2.39
184	T-complex protein 1, beta subunit	0	At5g20890	1.39
185	proline oxidase, mitochondrial precursor (osmotic stress-induced	0	At3g30775	1.45
186	linker histone protein, putative	1E-126	At1g14900	1.33
187	hypothetical protein	0	At1g27500	2.21

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188	ARF1-binding protein	0	At5g62010	1.58
189	putative protein	0	At5g16270	1.37
190	putative protein	1E-173	At5g13850	1.32
191	unknown protein	0	At1g09070	2.19
192	RAN2 small Ras-like GTP-binding nuclear protein (Ran-2)	0	At5g20020	1.30
193	phosphoprotein phosphatase (PPX-1)	0	At4g26720	1.42
194	nuclear protein-like	0	At5g64270	1.45
195	ornithine carbamoyltransferase precursor	0	At1g75330	1.41
196	unknown protein	0	At2g41650	1.67
197	putative protein	0	At5g17640	1.66
198	hypothetical protein	0	At1g57990	2.02
199	hypothetical protein	0	At4g15760	1.64
200	glycine-rich protein 2 (GRP2)	0	At4g38680	1.72
201	hypothetical protein	1E-113	At2g41780	2.60
202	RNA-binding protein, putative	8E-95	At3g20250	1.46
203	gda-1, putative	2E-15	At3g27090	1.46
204	beta-fructofuranosidase 1	0	At3g13790	1.32
205	26S proteasome subunit 4-like protein	0	At4g29040	1.51
206	putative protein	1E-59	At1g33980	1.42
207	hypothetical protein	0	At1g57680	2.66
208	unknown protein	0	At1g29980	1.98
209	60S ribosomal protein - like	0	At5g02870	1.39
210	REVOLUTA or interfascicular fiberless 1	0	At5g60690	1.34
211	RAC-like GTP-binding protein ARAC4	1E-180	At1g20090	1.78
212	unknown protein	2E-42	At3g07390	1.34
213	unknown protein	0	At5g65660	1.70
214	unknown protein	1E-154	At3g05040	1.52
215	putative DNA gyrase subunit A	1E-153	At3g10690	2.20
216	putative protein	0	At3g49170	1.53
217	eukaryotic cap-binding protein (gb|AAC17220.1)	0	At5g18110	1.41
218	phosphoethanolamine N-methyltransferase, putative	0	At1g73600	1.62
219	unknown protein	0	At2g30590	2.78
220	RAN1 small Ras-like GTP-binding nuclear protein (Ran-1)	0	At5g20010	1.46
221	putative protein	1E-104	At4g24290	1.32
222	putative auxin-regulated protein	0	At2g45210	1.33
223	adenylosuccinate synthetase	0	At3g57610	1.39
224	putative protein	0	At5g14530	2.70
225	putative ubiquitin activating enzyme E1 (ECR1)	0	At5g19180	1.63
226	putative mitochondrial processing peptidase	0	At3g02090	1.40
227	putative protein	0	At3g48530	1.55
228	putative protein	0	At3g48530	1.55
229	hypothetical protein	0	At1g20330	1.47
230	hypothetical protein	0	At4g02590	1.36
231	putative pyrophosphate-fructose-6-phosphate 1-phosphotransferase	0	At1g12000	1.49
232	putative receptor-like protein kinase	0	At2g02220	1.55
233	putative protein	1E-104	At4g02440	1.40
234	non-phototropic hypocotyl, putative	0	At1g30440	1.57

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235	histone deacetylase	0	At5g63110	1.36
236	putative protein	0	At5g66580	3.18
237	multicatalytic endopeptidase complex, proteasome precursor, beta	0	At4g31300	1.42
238	fibrillarin - like protein	6E-77	At4g25630	1.30
239	hypothetical protein	8E-45	At1g54060	1.36
240	histone H1, partial	0	At2g30620	1.58
241	hypothetical protein	0	At3g09030	1.45
242	enoyl-CoA hydratase - like protein	0	At4g31810	1.31
243	unknown protein	7E-12	At2g27080	1.51
244	myb-related transcription factor, putative	0	At3g23250	1.49
245	Alcohol Dehydrogenase	0	At1g77120	5.09
246	hypothetical protein	1E-132	At1g27590	1.38
247	unknown protein	0	At1g14710	1.36
248	putative receptor-like protein kinase	0	At2g13790	1.68
249	putative protein	0	At5g14550	1.39
250	HOMEOBOX PROTEIN KNOTTED-1 LIKE 4 (KNAT4)	1E-165	At5g11060	1.40
251	putative protein	1E-142	At5g15540	1.47
252	carbonyl reductase-like protein	7.4	At5g51030	2.17
253		1E-50	At1g53900	1.36
254	aspartate--tRNA ligase - like protein	0	At4g31180	1.62
255	unknown protein	1E-121	At3g06150	1.74
256	amino acid transporter protein-like	0	At5g65990	1.59
257	12-oxophytodienoate reductase (OPR1)	0	At1g76680	1.43
258	calnexin homolog	6E-25	At5g07340	1.39
259		0	At1g61100	2.06
260	homogentisate 1,2-dioxygenase	1E-78	At5g54080	2.01
261	glucosyltransferase -like protein	0	At4g34131	1.33
262	putative protein	0.36	At5g54890	1.35
263	hypothetical protein	0	At1g76070	1.31
264	putative protein	1E-179	At5g18310	1.56
265	DNA binding protein ACBF - like	0	At5g19350	1.36
266	hypothetical protein	0	At1g17210	1.69
267	putative protein	1E-111	At5g51220	1.46
268	RING finger protein	0	At3g61460	2.14
269	putative protein	0	At5g18580	1.32
270	putative protein kinase	0	At2g31010	1.35
271	chloroplast nucleoid DNA binding protein, putative	0	At1g01300	1.49
272	unknown protein	1E-143	At1g31130	1.40
273	splicing factor, putative	1E-16	At1g14650	1.56
274	putative TCP3 gb|AAC24010.1; similar to ESTs gb|T45419.1,	0	At1g53230	1.38
275	unknown protein	0	At1g72790	1.71
276	ribosomal protein S6 - like	0	At4g31700	1.38
277	auxin-resistance protein AXR1	0	At1g05180	1.36
278	putative protein	0	At5g11030	1.43
279	putative 60S acidic ribosomal protein P0	0	At3g09200	1.47
280	mismatch binding protein, putative	0	At3g24320	2.10
281	T-complex chaperonin protein , epsilon subunit	0	At1g24510	1.47

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282	putative protein	0	At4g24120	1.56
283	putative protein	4E-38	At5g53900	1.79
284	histidine transport protein (PTR2-B)	0	At2g02040	1.37
285	unknown protein	0	At3g10490	1.43
286	tubulin alpha-5 chain-like protein	0	At5g19770	1.60
287	putative non-LTR retroelement reverse transcriptase	0.006	At2g15510	4.71
288	unknown protein	1E-179	At2g41010	1.33
289	putative chloroplast outer envelope 86-like protein	0	At4g02510	1.45
290	serine/threonine-specific protein kinase NAK	0	At5g02290	1.56
291	unknown protein	0	At2g34680	1.45
292	hypothetical protein	0	At1g43170	1.69
293	phospholipase D, putative, 5' partial	0	At3g16785	1.50
294	CTP synthase-like protein	0	At1g30820	1.58
295	nitrilase 2	0	At3g44300	1.84
296	putative mitogen activated protein kinase kinase	0	At3g04910	1.34
297	putative protein	0	At4g27450	1.40
298	Phospholipase like protein	0	At4g38550	1.90
299	endomembrane-associated protein	3E-41	At4g20260	1.83
300	leucine-rich receptor-like protein kinase, putative	0	At1g72180	2.13
301	putative protein	0.81	At4g25930	1.54
302	WD-40 repeat protein MSI1 (sp|O22467); also highly similar to G1/S	0	At5g58230	1.72
303	oxysterol-binding protein - like	1E-171	At5g59420	1.31
304	putative protein	1E-178	At4g21840	1.40
305	blue copper binding protein	1E-50	At5g20230	2.30
306	UV-damaged DNA-binding protein- like	0.000000006	At4g21100	1.46
307	fatty acid hydroxylase (FAH1)	0	At2g34770	1.96
308	putative thymidine kinase	0	At3g07800	8.44
309	hypothetical protein	0	At1g79380	1.41
310	unknown protein	0	At2g15860	1.36
311	flower pigmentation protein ATAN11	0	At1g12910	1.41
312	hypothetical protein	0	At1g56290	1.33
313	putative protein	0	At3g62630	1.38
314		0	At1g61140	1.42
315	unknown protein	0	At3g16310	1.49
316	putative glucosyl transferase	0	At2g36800	1.36
317	putative protein	0	At4g25170	1.92
318	hypothetical protein	9E-39	At4g00450	1.36
319	glutathione S-transferase	0	At2g30860	1.49
320	unknown protein, 3' partial	0	At3g15095	1.42
321	unknown protein	0	At3g21080	1.31
322	TCH4 protein (gb|AAA92363.1)	0	At5g57560	1.92
323	putative protein	0	At3g61600	1.34
324	receptor-like kinase, putative	0	At3g23750	2.06
325	putative 2,3-bisphosphoglycerate-independent phosphoglycerate	0	At1g09780	1.34
326	putative protein	0	At5g14250	1.51
327	DnaJ homologue (gb|AAB91418.1|)	0	At5g06910	2.32
328	hypothetical protein	0	At1g33250	1.35
329	unknown protein	0	At2g19800	1.81

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330	aspartate carbamoyltransferase precursor (aspartate	3E-84	At3g20330	1.49
331	hypothetical protein	0	At1g16520	1.35
332	unknown protein	5E-19	At1g48620	1.33
333	putative protein	1E-18	At4g35750	1.39
334	hypothetical protein	1E-55	At3g13620	1.79
335	RNA helicase, DRH1	1E-179	At3g01540	1.56
336	putative 3-oxoacyl [acyl-carrier protein] reductase	0	At1g24360	1.42
337	putative cellular apoptosis susceptibility protein	1E-142	At2g46520	1.43
338	hypothetical protein	0	At1g01540	1.31
339	starch branching enzyme II	2E-61	At2g36390	1.36
340	40S ribosomal protein - like	0	At5g15200	1.32
341	putative protein	0	At4g13640	1.33
342	putative protein	0	At3g45970	3.22
343	hypothetical protein	0	At1g66160	1.31
344	AP2 domain containing protein RAP2.3	0.000000002	At3g16770	1.51
345	putative protein	1E-47	At5g02880	1.32
346	NADH-dependent glutamate synthase	0	At5g53460	2.25
347	ARGININE/SERINE-RICH SPLICING FACTOR RSP31	4E-59	At3g61860	1.31
348	hypothetical protein	1E-134	At1g55880	1.37
349	translation initiation factor eIF3 - like protein	6E-77	At4g20980	1.45
350	putative serine/threonine protein phosphatase catalytic subunit,	0	At2g42500	1.38
351	unknown protein	1E-105	At1g33480	1.91
352	COP1-interacting protein CIP8	0	At5g64920	1.40
353	nonphototropic hypocotyl 1	6E-16	At3g45780	1.47
354	putative protein	1E-78	At5g10860	1.32
355	putative protein	0	At5g19750	1.37
356	putative protein	1E-127	At3g52500	1.39
357	putative protein	0	At4g10280	1.76
358	cytochrome P450 monooxygenase	0	At4g31500	1.35
359	ethylene responsive element binding factor 1 (frameshift !)	1E-104	At4g17500	1.33
360	hypothetical protein	0	At1g17620	1.37
361	unknown protein	1E-123	At3g07390	1.42
362	putative protein kinase	0	At3g02880	1.46
363	DNA repair protein RAD23 homolog	0	At5g38470	1.42
364	GTP-binding protein - like	1E-25	At5g03520	1.57
365	putative protein	0	At3g63500	1.40
366	putative adenylate kinase	4E-19	At2g39270	1.37
367	protein kinase - like	6E-46	At5g59010	1.42
368	unknown protein	0	At3g04630	1.58
369		0	At1g73490	1.32
370	putative phospholipase D	0	At3g15730	1.51
371	importin alpha	1E-115	At3g06720	1.45
372	RING-H2 finger protein RHF2a	0	At5g22000	1.43
373	putative protein	2E-93	At4g19160	1.30
374	putative protein	0	At4g32440	1.41
375	putative protein phosphatase type 2C	0	At3g15260	1.61
376	putative protein	0	At5g39890	1.31

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377	ribosomal protein	0	At4g16720	1.42
378	dormancy-associated protein	9E-15	At1g28330	2.01
379	auxin-inducible gene (IAA2)	0	At3g23030	1.65
380	unknown protein	5E-19	At1g76010	1.54
381	protein kinase ADK1-like protein	1.4	At4g28540	1.96
382	putative protein	0	At4g24210	1.36
383	hypothetical protein	0	At1g79530	1.40
384	putative trehalose-6-phosphate synthase	0	At1g68020	1.45
385	adenylate kinase	0	At5g63400	1.39
386	putative proline-rich protein precursor	0	At1g73840	1.56
387	putative protein	5E-87	At5g14370	1.37
388	hypothetical protein	0	At4g33290	1.70
389	cytochrome P450 monooxygenase (CYP71B3)	0	At3g26220	1.32
390	TMV resistance protein N - like	0	At4g19530	1.50
391	hypothetical protein	9E-70	At1g54830	1.33
392	3-ketoacyl-CoA thiolase	0	At2g33150	1.87
393	putative protein	0	At3g54350	1.35
394	hypothetical protein	1E-170	At4g02680	1.36
395	putative bHLH transcription factor	0	At2g46510	1.35
396	RNA-binding protein, putative	5E-84	At3g26420	1.55
397	putative lectin	3E-20	At3g09190	1.67
398	xyloglucan endotransglycosylase, putative	0	At3g23730	2.85
399	unknown protein	2E-33	At2g41170	1.32
400	putative protein	3E-78	At3g57150	1.67
401	putative glucose regulated repressor protein	0	At2g25490	1.81
402	putative AP2 domain containing protein RAP2.4 gi|2281633; similar	1E-150	At1g78080	1.82
403	putative sulfate transporter	0	At1g80310	1.51
404	G protein alpha subunit 1 (GPA1)	0	At2g26300	1.44
405	protochlorophyllide reductase precursor	0	At4g27440	2.39
406	Shaggy related protein kinase tetha	0	At4g00720	1.52
407	putative protein kinase	0	At3g01300	1.49
408	RNA-binding protein-like protein	0	At3g47160	1.31
409	unknown protein	1E-150	At5g24670	1.47
410	zinc finger protein ZFP8	1E-144	At2g41940	1.42
411	GTP binding protein beta subunit	0	At4g34460	1.54
412	copia-like retroelement pol polyprotein	0	At2g22680	1.40
413	CONSTANS-like B-box zinc finger protein-like	0	At5g57660	1.36
414	unknown protein	3E-71	At3g10640	1.33
415	putative protein	0	At4g24690	1.91
416	NADH dehydrogenase	1E-124	At5g08530	1.42
417	unknown protein	0	At1g73820	1.35
418	monosaccharide transport protein, STP4	0.000000008	At3g19930	1.58
419	globulin-like protein	0	At1g07750	1.61
420	putative transitional endoplasmic reticulum ATPase	2E-58	At3g09840	1.51
421	putative monodehydroascorbate reductase	0	At1g63940	1.39
422	anthranilate phosphoribosyltransferase-like protein	0	At3g57880	1.42
423	H+-transporting ATP synthase chain 9 - like protein	6E-25	At4g32260	1.83
424	hypothetical protein	0	At1g02810	2.31

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425	calmodulin-like protein	3E-63	At2g41410	1.52
426	putative protein	0	At5g15350	2.75
427	glutathione S-transferase	0	At2g30870	1.54
428	putative SWI/SNF complex subunit SW13	1E-138	At2g33610	1.32
429	MAP kinase kinase 2	0	At4g29810	1.39
430	adenosylhomocysteinase	1E-134	At4g13940	2.07
431	putative protein	0	At5g27760	1.40
432	unknown protein	0	At2g47450	1.67
433	putative protein	0	At4g33050	2.20
434	50S ribosomal protein L12-C	1E-138	At3g27850	1.38
435	26S proteasome AAA-ATPase subunit RPT4a (gb|AAF22524.1)	0	At5g43010	1.40
436	unknown protein	0.84	At3g01690	1.31
437	lipid transfer protein; glossy1 homolog	0	At5g57800	1.39
438	indoleacetic acid (IAA)-inducible gene (IAA7)	0.0000001	At3g23050	1.52
439	histone H2B - like protein	0	At5g59910	2.16
440	putative RNA helicase	0	At3g06480	1.47
441	unknown protein	8E-64	At1g19310	1.44
442	unknown protein	4E-96	At2g18440	1.38
443	unknown protein	0	At1g68220	1.59
444	unknown protein	1E-142	At2g20570	1.35
445	putative replication factor	1E-124	At1g21690	3.30
446	U2 snRNP auxiliary factor, small subunit	0	At5g42820	1.55
447	replication factor C - like	0	At5g27740	1.45
448	nuclear receptor binding factor-like protein	0	At3g45770	1.62
449	putative glycosyl transferase	0	At1g24170	2.39
450	histone H2A-like protein	4E-53	At5g27670	1.62
451	putative protein	1E-125	At5g48960	1.43
452	hypothetical protein	0	At1g53740	1.42
453	splicing factor - like protein	0	At3g53500	1.39
454	unknown protein	0	At1g50510	1.32
455	Fe(II) transport protein	0	At4g19690	1.37
456	hypothetical protein	0	At1g61730	1.43
457	unknown protein	0.000000007	At2g47440	2.50
458	cold-regulated protein COR6.6 (KIN2)	0	At5g15970	3.03
459	putative cytochrome C	0	At1g22840	1.30
460	unknown protein	0	At1g68580	2.13
461	putative Ser/Thr protein kinase	0	At1g16270	1.37
462	pseudogene	1E-138	At2g25970	2.15
463	unknown protein	0	At3g06380	1.67
464	Tic22, putative	3E-84	At3g23710	2.14
465	unknown protein	0	At1g09250	1.55
466	hypothetical protein	0	At1g72930	1.91
467	hypothetical protein	2E-18	At1g68820	1.43
468	histone H1	0	At2g18050	1.75
469	unknown protein	0	At1g08630	1.45
470	unknown protein, 5'partial	0	At3g18035	3.31
471	unknown protein	0	At1g04140	1.37
472	HAL3A protein	0	At3g18030	1.43

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473	phi-1-like protein		0	At5g64260	3.38
474	hypothetical protein		0	At1g12770	1.35
475	pollen specific protein SF21		0	At5g56750	1.45
476	cysteine proteinase inhibitor like protein		1E-159	At4g16500	1.33
477	20S proteasome subunit C8 (PAG1/PRC8 ARATH)		1E-130	At2g27020	1.36
478	nodulin-like protein		1E-99	At1g75500	1.34
479	hypothetical protein		0	At1g72900	2.04
480	hypothetical protein		0	At2g35230	1.42
481	arm repeat containing protein homolog		0	At3g46510	1.40
482	putative protein		0	At5g67480	1.76
483	putative leucyl-tRNA synthetase		1E-118	At1g09620	1.52
484	Putative UDP-glucose glucosyltransferase		1E-164	At1g22400	2.34
485	alanine aminotransferase, putative		0	At1g17290	1.66
486	26S proteasome AAA-ATPase subunit RPT6a		0	At5g19990	1.36
487	Ruv DNA-helicase-like protein		0	At5g22330	1.59
488	small nuclear ribonucleoprotein, putative		0	At1g65700	1.33
489	unknown protein		0	At2g38310	2.79
490	protein phosphatase type 1 PP1BG		3E-91	At4g11240	1.51
491	hypothetical protein		3E-41	At2g43410	2.10
492	putative protein		0	At5g58600	1.42
493	nodulin-like protein		0	At1g80530	2.07
494	putative protein		0	At5g56170	1.65
495	dihydroxyacetone kinase, putative		1E-167	At3g17770	1.67
496	ribsomal protein - like		1E-155	At5g09770	1.44
497	101 kDa heat shock protein; HSP101-like protein		0	At5g57710	1.34
498	unknown protein		0	At5g51340	1.48
499	unknown protein		0	At3g05730	1.46
500	putative protein		1.7	At5g67570	2.60
501	mitochondrial chaperonin (HSP60)		0	At2g33210	1.75
502	putative protein		1E-177	At3g63270	1.34
503	growth factor like protein		0	At4g12720	1.78
504	RNA helicase, putative		0	At3g19760	1.54
505	pseudogene		1E-142	At2g34760	1.81
506	hypothetical protein		0	At3g21740	1.52
507	shaggy-like kinase beta		0	At3g61160	1.36
508	unknown protein		1E-165	At1g20100	1.35
509	24-sterol C-methyltransferase		1E-143	At5g13710	1.41
510	WD-40 repeat protein (MSI3)		0	At4g35050	4.89
511	hypothetical protein		0	At1g67120	1.51
512	putative protein (fragment)		0	At5g14930	1.46
513	putative protein		0.000001	At5g54180	1.78
514	hypothetical protein		1E-126	At1g20570	1.43
515	calcium-dependent protein kinase		0	At5g66210	2.96
516	nitrilase 2		1E-127	At3g44300	1.88
517	methionyl-tRNA synthetase - like protein		1E-173	At4g13780	1.33
518	putative protein		0	At4g24230	1.58
519	putative protein		2E-76	At5g19330	1.33
520	caffeoyl-CoA O-methyltransferase - like protein		1E-166	At4g34050	1.41
521	putative DNA binding protein		0	At4g27000	1.43

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522	unknown protein	0	At1g55270	1.40
523	carbamoyl phosphate synthetase large chain (carB)	0	At1g29900	1.50
524	hypothetical protein	0.006	At4g02680	2.73
525	putative RNA helicase	0	At3g22310	1.53
526	molybdopterin synthase sulphurylase (gb|AAD18050.1)	0	At5g55130	1.77
527	inner mitochondrial membrane protein, putative	0	At1g17530	1.55
528	putative protein kinase	0	At3g08760	1.90
529	putative JUN kinase activator protein	0	At1g22920	1.42
530	thaumatin, putative	0	At1g75800	1.56
531	DNA-binding protein	0	At3g14230	1.54
532	unknown protein	0	At2g01710	1.34
533	putative calcium binding protein	0	At2g43290	1.57
534	class 1 non-symbiotic hemoglobin (AHB1)	5E-93	At2g16060	1.86
535	glycine-rich RNA binding protein, putative	2E-52	At3g23830	1.38
536	unknown protein	2E-37	At2g01190	1.30
537	hydoxyethylthiazole kinase, putative	2E-71	At3g24030	1.35
538	putative protein translocase	0	At2g37410	1.51
539	putative protein	0.047	At5g61560	1.31
540	hypothetical protein	0.067	At1g35600	1.56
541	ethylene-insensitive 3	0	At3g20770	1.50
542	lipoxygenase AtLOX2	0	At3g45140	1.57
543	putative phosphatidic acid phosphatase	0	At2g01180	1.85
544	unknown protein	0.00005	At1g80860	1.30
545	unknown protein	2E-15	At3g28180	1.64
546	unknown protein	0	At3g02550	4.01
547	putative protein	0.019	At5g22260	1.95
548	actin - like protein	1E-180	At3g60830	1.36
549	DEAD-box protein abstrakt	0	At5g51280	1.53
550	putative DNA polymerase epsilon catalytic subunit	1.9	At2g27120	2.87
551	unknown protein	6E-59	At5g48020	1.40
552	protein kinase C inhibitor-like protein	0	At3g56490	1.58
553	putative PRP19-like spliceosomal protein	0	At2g33340	1.70
554	germin-like protein	0	At1g72610	1.67
555	putative protein	0.00001	At5g10050	1.32
556	putative protein	0	At4g34950	1.96
557	zinc finger protein	0	At5g66730	1.37
558	chaperonin gamma chain - like protein	1E-176	At5g26360	1.67
559		7E-15	At4g07410	1.42
560	putative DNA-binding protein	0	At4g12080	1.40
561	beta-glucosidase, putative	0	At1g52400	1.66
562	hypothetical protein	1E-44	At2g23140	1.66
563	homeobox protein	1E-43	At3g61150	1.63
564	glycine-rich protein	0	At4g36020	1.82
565	unknown protein	0	At3g01460	1.37
566	hypothetical protein	1E-134	At4g28190	1.40
567	predicted protein	5E-37	At4g32010	1.34
568	N-myristoyl transferase	1E-157	At5g57020	1.37
569	putative protein	0	At4g36780	1.61

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570	unknown protein	0.15	At5g48240	1.64
571	unknown protein	0	At1g21630	1.55
572	unknown protein	1E-102	At1g07360	1.74
573	lysyl-tRNA synthetase	1E-96	At3g11710	1.38
574	unknown protein	0	At3g07780	1.51
575	tryptophan synthase beta chain 1 precursor (sp|P14671)	1E-102	At5g54810	1.55
576	putative protein	8E-98	At4g25620	1.81
577	RuvB DNA helicase-like protein	0	At5g67630	1.32
578	putative pectin methylesterase	0	At3g14310	1.43
579	putative cytidine deaminase	0	At2g19570	1.41
580	hypothetical protein	0	At3g12400	1.42
581	1-aminocyclopropane-1-carboxylate synthase -like protein	0	At4g26200	1.54
582	peroxidase	3E-88	At2g38380	2.11
583	2-oxoglutarate dehydrogenase, E1 component	0	At5g65750	1.44
584	xylosidase	0	At5g49360	1.93
585	ethylene responsive element binding factor 4	0	At3g15210	1.70
586	putative protein	1.6	At5g46650	3.54
587	eukaryotic protein synthesis initiation factor 4A	0	At3g13920	1.35
588		0	At1g76970	2.34
589	hypothetical protein	0	At1g19380	1.54
590	unknown protein	0	At5g49640	1.78
591	putative xyloglucan-specific glucanase	0	At2g01850	1.58
592	similar to nucellin gb|AAB96882.1	1E-106	At1g49050	1.50
593	unknown protein	0	At3g29390	1.33
594	putative protein	0	At3g62190	1.58
595	putative malate dehydrogenase	0	At1g04410	1.34
596	putative isocitrate lyase	1E-153	At3g21720	3.08
597	DNA-binding protein	1E-160	At3g14230	1.48
598	histone H4-like protein	0	At3g46320	2.55
599	putative dehydrogenase	0	At1g71170	1.47
600	alanine--tRNA ligase, putative	0	At1g50200	1.38
601	oligopeptidase A - like protein	1E-172	At5g10540	1.43
602	putative protein	0	At5g62620	1.32
603	permease	0	At5g49990	1.30
604	DEAD BOX RNA helicase RH15	1E-129	At5g11200	1.40
605	lipoamide dehydrogenase precursor	1E-128	At3g17240	1.38
606	hypothetical protein	0	At1g15170	1.75
607	xyloglucan endo-1,4-beta-D-glucanase (XTR-6)	0	At4g25810	1.95
608	histone H2B like protein (emb|CAA69025.1)	7E-34	At5g22880	1.91
609	S-receptor kinase homolog 2 precursor	1.3	At5g60900	2.61
610	60S ribosomal protein L2	7E-48	At2g18020	1.58
611	unknown protein	0	At1g23030	1.98
612	zinc finger protein, putative	0	At1g34370	1.51
613	putative protein	0.00000003	At4g05150	1.38
614	aldose 1-epimerase - like protein	5E-25	At3g47800	1.88
615	cinnamoyl-CoA reductase - like protein	0	At5g58490	1.35
616	putative NADP-dependent glyceraldehyde-3-phosphate dehydrogenase	0	At2g24270	1.43

617	isp4 like protein	0	At4g16370	1.77
618	putative protein	0	At4g08350	1.32
619	CALMODULIN-RELATED PROTEIN 2, TOUCH-INDUCED (TCH2)	0	At5g37770	1.55
620	20S proteasome subunit PAD2 (gb|AAC32059.1)	0	At5g66140	1.50
621	glucosidase II alpha subunit	0	At5g63840	1.35
622	putative GAR1 protein	0	At3g03920	1.74
623	putative protein	3E-45	At5g08450	1.79
624	glutamate dehydrogenase (EC 1.4.1.-) 1 (pir||S71217)	0	At5g18170	1.47
625	putative protein	0	At5g06660	1.32
626	Nonclathrin coat protein gamma - like protein	1E-143	At4g34450	1.43
627	unknown protein	0	At3g17860	1.60
628	similar to senescence-associated protein	0	At2g23810	1.59
629	putative protein	0	At5g60420	1.31
630	unknown protein	0	At1g28260	1.36
631	shaggy-like protein kinase etha (EC 2.7.1.-)	0	At4g18710	1.37
632	putative 26S protease regulatory subunit 6A	0	At1g09100	1.47
633	unknown protein	0	At3g21140	1.49
634	dynamin-like protein	0	At2g14120	1.40
635	scarecrow-like 1	2E-47	At1g21450	1.75
636	unknown protein	7E-40	At3g02710	1.30
637	putative protein	0	At5g50670	1.41
638	helicase-like protein	1E-108	At5g44800	1.50
639	dynamin-like protein 4 (ADL4)	1E-100	At3g60190	1.32
640	unknown protein	0	At3g12790	1.31
641	putative Tub family protein	0	At2g47900	1.37
642	putative protein	1E-119	At5g13020	1.33
643	alanine aminotransferase, putative	1E-147	At1g17290	1.36
644	SCARECROW-like protein	0	At4g36710	1.49
645	alpha galactosyltransferase-like protein	0	At3g62720	3.26
646	putative protein	0	At4g31980	1.32
647	putative protein	1E-124	At3g56480	1.34
648	histone acetyltransferase HAT B	0	At5g56740	2.36
649	putative phosphoribosyl pyrophosphate synthetase	3E-97	At2g44530	1.45
650	AIG1	1E-130	At1g33960	1.45
651	hypothetical protein	0	At4g22190	1.69
652	hypothetical protein	0	At1g26180	1.33
653	putative protein	4E-84	At5g59000	1.61
654	hypothetical protein	0	At2g27660	1.66
655	unknown protein	0	At1g33400	1.38
656	helicase-like protein	0	At5g44800	1.63
657	putative protein	0	At5g44920	1.43
658	putative RNA-binding protein	0	At1g22910	2.13
659	meiosis specific - like protein	0	At5g02820	2.62
660	isocitrate dehydrogenase - like protein	0	At5g14590	1.43
661	hypothetical protein	1E-139	At1g15500	1.63
662	putative protein	0.34	At5g52270	1.38
663	ABC transporter-like protein	0	At5g06530	1.63
664	heat-shock protein 90, putative	0	At1g27640	1.48

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665	unknown protein	0	At3g07220	1.33

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Tab 5: Arabidopsis genes 1.3 times (1/ratio) or more repressed in E2Fa/Dpa plants

	Gene name	E-value	MIPS accession Number	Ratio
1	putative glutathione peroxidase	0	At2g31570	0.51
2	phenylalanine ammonia lyase (PAL1)	0	At2g37040	0.65
3	unknown protein	0	At1g04040	0.62
4	putative protein	0	At4g25340	0.52
5	water channel - like protein	1E-129	At4g23400	0.70
6	catalase	0	At4g35090	0.46
7	stearoyl-ACP desaturase	2E-11	At2g43710	0.54
8	putative oligopeptide transporter	0	At4g10770	0.37
9	putative chloroplast 50S ribosomal protein L28	0	At2g33450	0.73
10	ferredoxin--NADP reductase precursor, putative	0	At1g20020	0.64
11	3-beta-hydroxysteroid dehydrogenase	1E-44	At2g26260	0.73
12	putative alanine aminotransferase	1E-127	At1g70580	0.51
13	hypothetical protein	4E-99	At1g56500	0.66
14	putative protein	0	At5g21940	0.64
15	putative protein	1E-158	At5g26970	0.70
16	actin depolymerizing factor 4 - like protein	0	At5g59890	0.66
17	hypothetical protein	7E-72	At3g45160	0.50
18	transporter-like protein	0.0000001	At3g53960	0.68
19	nicotianamine synthase (dbj|BAA74589.1)	0	At5g04950	0.35
20	cytochrome P450 monooxygenase (CYP83A1)	0	At4g13770	0.39
21	unknown protein	0	At2g29660	0.77
22	hypothetical protein	0	At3g12580	0.56
23	unknown protein	0	At5g64130	0.52
24	putative protein	0	At3g61870	0.73
25	fructose-bisphosphate aldolase - like protein	0	At4g26530	0.17
26	lectin like protein	1E-124	At4g19840	0.74
27	unknown protein	0	At1g28140	0.72
28	feebly-like protein	0	At3g01420	0.73
29	beta-fructosidase	1E-105	At1g62660	0.38
30	unknown protein	0.000001	At1g15350	0.77
31				0.70
32				0.66
33				0.67
34	peptidylprolyl isomerase ROC1	0	At4g38740	0.76
35	hypothetical protein	1E-36	At2g06010	0.74
36	putative protein	1E-114	At4g30490	0.50
37	3-isopropylmalate dehydrogenase	0	At5g14200	0.61
38	putative copper/zinc superoxide dismutase	1E-93	At2g28190	0.77
39	putative myo-inositol 1-phosphate synthase	0	At2g22240	0.68
40	putative enolase (2-phospho-D-glycerate hydroylase)	0	At2g29560	0.70
41	unknown protein	0	At5g43750	0.40
42	putative protein	1E-22	At4g32330	0.68
43	putative ferredoxin-thioredoxin reductase	0	At2g04700	0.75
44	hypothetical protein	1.3	At3g23290	0.59
45	putative cellulose synthase	0	At2g32530	0.58
46	putative protein	0	At5g43850	0.54

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47	putative protein	0	At5g03010	0.58
48	hypothetical protein	0	At1g78140	0.61
49	unknown protein	0	At1g72590	0.35
50	hypothetical protein	0	At1g54450	0.59
51	hypothetical protein	0	At1g19110	0.73
52	endo-beta-1,4-glucanase, putative	0	At1g75680	0.70
53	unknown protein	0	At1g63010	0.76
54	hypothetical protein	2E-58	At4g24700	0.57
55	glyoxalase II	0	At1g53580	0.65
56	putative protein	0	At3g52370	0.53
57	unknown protein	0	At1g80280	0.57
58	protein phosphatase ABI1	0	At4g26080	0.71
59	33 kDa polypeptide of oxygen-evolving complex (OEC) in photosystem	1E-115	At5g66570	0.65
60	beta-xylosidase	1E-163	At5g64570	0.55
61	GDP-mannose pyrophosphorylase	0	At2g39770	0.62
62	peroxidase ATP20a (emb|CAA67338.1)	0	At5g14130	0.67
63	putative glutathione transferase	0	At1g17190	0.71
64	putative protein	0	At4g38080	0.75
65		1E-179	At1g61190	0.70
66	50S ribosomal protein L24, chloroplast precursor	0	At5g54600	0.76
67	unknown protein	1E-179	At1g68260	0.55
68	subtilisin-like serine proteinase, putative, 3' partial	0	At3g14067	0.62
69	putative protein	0	At4g23890	0.59
70	unknown protein	0	At3g01690	0.70
71	putative protein	0	At3g56290	0.30
72	unknown protein	0	At2g39450	0.67
73	unknown protein	0	At5g64130	0.66
74	putative protein	0	At4g30140	0.54
75	ribulose bisphosphate carboxylase small chain 3b precursor (RuBisCO	1E-145	At5g38410	0.54
76				0.66
77				0.71
78	Myb DNA binding protein -like	0	At3g46130	0.75
79	putative 2-cys peroxiredoxin	0	At3g11630	0.64
80	putative trypsin inhibitor	0	At1g73260	0.59
81	O-methyltransferase	1E-127	At5g54160	0.62
82	hypothetical protein	2E-30	At1g29270	0.73
83	RP19 gene for chloroplast ribosomal protein CL9	9E-67	At3g44890	0.68
84	putative phosphoglyceride transfer protein	1E-178	At4g08690	0.57
85	putative protein	0	At5g63530	0.53
86	putative protein	0	At5g38720	0.68
87	hypothetical protein	0	At1g72030	0.68
88	unknown protein	9E-21	At5g09990	0.67
89	zinc finger protein ZAT7	0	At3g46090	0.73
90	putative nodulin	0	At3g05180	0.64
91	putative wound-induced basic protein	1E-160	At3g07230	0.75
92	hypothetical protein	0	At4g02920	0.38
93	putative protein	1E-154	At5g62220	0.73
94	myosin heavy chain-like protein	0	At3g16000	0.50
95	unknown protein	0	At1g09610	0.76
96	arabinogalactan protein - like	0	At5g03170	0.71

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97	biotin carboxyl carrier protein of acetyl-CoA carboxylase precursor	0	At5g16390	0.69
98	centrin	0	At3g50360	0.74
99	vegetative storage protein Vsp1	0	At5g24780	0.48
100	protein kinase, putative	1E-61	At1g52310	0.63
101	unknown protein	1E-132	At2g42760	0.63
102	phenylalanine ammonia lyase (PAL1)	0	At2g37040	0.72
103	UDP rhamnose-anthocyanidin-3-glucoside rhamnosyltransferase - like	0	At4g27560	0.45
104	unknown protein	0	At2g17500	0.54
105	NAC domain protein, putative	0	At1g01720	0.72
106	ubiquitin-conjugating enzyme-like protein	2E-24	At5g56150	0.41
107	putative RNA-binding protein	1E-136	At2g37220	0.72
108	Overlap with bases 87,142-90,425 of 'IGF' BAC clone F9K20, accession	0	At1g78570	0.52
109	hypothetical protein	1E-105	At2g04040	0.52
110	lsp4-like protein	0.44	At5g64410	0.39
111	ids4-like protein	0	At5g20150	0.58
112	unknown protein	3E-98	At1g44000	0.67
113	R2R3-MYB transcription factor	0	At3g50060	0.66
114	putative hexose transporter	0	At4g02050	0.68
115	one helix protein (OHP)	0	At5g02120	0.57
116	UDP-glucose dehydrogenase-like protein	0	At5g15490	0.74
117	putative protein	0	At3g54260	0.63
118	putative L5 ribosomal protein	0	At4g01310	0.75
119	putative myosin heavy chain	0	At2g37080	0.61
120	clpB heat shock protein-like	0	At5g15450	0.57
121		4E-71	At1g52510	0.66
122	beta-fructosidase, putative	0	At1g12240	0.55
123	hypothetical protein	0	At1g47670	0.69
124	putative protein	3E-36	At5g25890	0.75
125	predicted protein	1E-108	At4g31390	0.73
126	putative phospholipase	0	At2g39420	0.66
127	ATP-dependent transmembrane transporter, putative	0	At1g51460	0.74
128	H+-transporting ATP synthase-like protein	0	At4g09650	0.64
129	putative protein	0	At4g29590	0.77
130	unknown protein	0	At3g02640	0.49
131	phosphoenolpyruvate carboxylase (PPC)	0	At3g14940	0.77
132	pollen allergen-like protein	0	At1g24020	0.28
133	putative AUX1-like permease	0	At1g77690	0.73
134	putative protein	1E-127	At4g39730	0.49
135	homeobox-leucine zipper protein ATHB-12	0	At3g61890	0.24
136	putative protein	0	At5g10160	0.53
137	unknown protein	0	At1g71480	0.56
138	putative violaxanthin de-epoxidase precursor (U44133)	0	At1g08550	0.70
139	nClpP5, putative	0	At1g49970	0.68
140	hypothetical protein	0	At1g65260	0.57
141	putative protein	1E-135	At3g52360	0.38
142	putative protein	0	At5g26260	0.50
143		0	At1g25170	0.66
144	hypothetical protein	0	At1g79550	0.65
145	tubulin beta-2/beta-3 chain (sp|P29512)	2E-21	At5g62700	0.61

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146	eukaryotic translation initiation factor 4E, putative	0	At1g29550	0.64
147	transport inhibitor response 1, putative	1E-175	At1g12820	0.77
148	osmotin precursor	1E-110	At4g11650	0.74
149	putative glutathione S-transferase TSI-1	0	At1g10360	0.72
150	protein ch-42 precursor, chloroplast	0	At4g18480	0.76
151	omega-3 fatty acid desaturase	0.000002	At2g29980	0.73
152	unknown protein	0	At2g44670	0.57
153	putative protein	0	At3g55330	0.51
154	putative calmodulin	0	At3g51920	0.55
155	plastid ribosomal protein L34 precursor, putative	1E-140	At1g29070	0.69
156	putative protein	0	At5g67070	0.66
157	putative 2Fe-2S iron-sulfur cluster protein	0	At3g16250	0.69
158	hypothetical protein	0	At1g42970	0.69
159	hypothetical protein	3E-69	At3g14190	0.60
160		1E-122	At1g77090	0.70
161	putative protein	0	At3g48420	0.42
162	actin 3	0	At2g37620	0.64
163	OEP8 like protein	4E-38	At4g15800	0.73
164	putative Ras-like GTP-binding protein	0	At3g09910	0.71
165	sulfolipid biosynthesis protein SQD1	0	At4g33030	0.68
166	oleosin isoform	0	At3g27660	0.61
167	acyl-CoA synthetase, putative	0	At1g64400	0.59
168	putative protein	1E-147	At3g61060	0.50
169	hypothetical protein	1E-117	At1g56200	0.64
170	putative protein	0	At4g13500	0.53
171	cinnamoyl CoA reductase, putative	0	At1g80820	0.72
172	hypothetical protein	1E-157	At4g28410	0.10
173	hypothetical protein	0	At1g54030	0.68
174	putative DNA-binding protein, GT-1	0	At3g25990	0.10
175	germin-like protein	0.0003	At3g05950	0.49
176	putative glutathione S-transferase	0	At2g29480	0.70
177	arabinogalactan-protein (gb|AAC77823.1)	0.000001	At5g64310	0.61
178	periaxin - like protein	1E-151	At5g09530	0.71
179	zeaxanthin epoxidase precursor	0	At5g67030	0.52
180	putative photosystem I reaction center subunit IV	0	At2g20260	0.70
181	putative 60S ribosomal protein L18A	0	At3g14600	0.74
182	putative ethylene response element binding protein (EREBP)	0	At2g44840	0.72
183	unknown protein	0	At2g21970	0.50
184	RNA-binding protein cp33 precursor	0	At3g52380	0.73
185	unknown protein	1E-152	At2g34460	0.62
186	CONSTANS-like 1	1E-179	At5g15850	0.60
187	unknown protein	0	At1g75100	0.77
188		9E-66	At1g15990	0.57
189	unknown protein	0	At2g21960	0.46
190	unknown protein	0	At1g66330	0.69
191	putative protein	0	At4g26630	0.68
192	unknown protein	1E-99	At3g28230	0.72
193	hypothetical protein	1E-65	At1g55910	0.65
194	putative Na+-dependent inorganic phosphate cotransporter	0	At2g29650	0.52
195	hypothetical protein	4E-23	At1g02330	0.71
196	hypothetical protein	0	At1g29700	0.55

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197	putative flavonol 3-O-glucosyltransferase	0	At2g18560	0.62
198	lycopene epsilon cyclase	0	At5g57030	0.60
199	hypothetical protein	0	At3g09150	0.75
200	putative protein	1E-150	At1g31710	0.50
201	hypothetical protein	0	At1g78850	0.69
202	putative protein	0	At4g32770	0.75
203	putative protein	2E-77	At4g22890	0.75
204	ripening-related protein - like	0	At5g20740	0.59
205	putative peroxidase ATP12a	0	At1g05240	0.65
206	hypothetical protein	7E-18	At4g01050	0.77
207	V-ATPase subunit G (vag2 gene)	0.0004	At4g23710	0.61
208	hypothetical protein	0	At1g58080	0.75
209	putative protein	2E-94	At5g19190	0.51
210	hypothetical protein	0	At1g48850	0.69
211	putative protein	0	At4g38800	0.75
212	similar to polygalacturonase-like protein emb|CAA66811; similar to	0	At1g10640	0.28
213	putative glutathione S-transferase	0	At2g02390	0.73
214	putative calcium-binding EF-hand protein	3E-78	At2g33380	0.69
215	unknown protein	1E-113	At1g64680	0.57
216	unknown protein	0	At3g15660	0.58
217	putative protein	0	At5g22080	0.74
218	high mobility group protein 2-like	2E-24	At3g51880	0.71
219	similar to late embryogenesis abundant proteins	4E-50	At2g44060	0.61
220	putative protein	0	At4g34600	0.74
221	putative protein	2E-31	At5g52060	0.48
222	NADPH oxidoreductase, putative	0	At1g75280	0.53
223	hypothetical protein	0	At1g16720	0.62
224	unknown protein	0	At3g28130	0.75
225	glutaredoxin	0	At4g15690	0.73
226	putative protein	0.42	At3g47590	0.66
227	putative protein	0	At4g26630	0.70
228	putative polyprotein	1E-139	At4g04410	0.76
229	MTN3-like protein	0	At3g48740	0.49
230	hypothetical protein	0	At1g32900	0.38
231	unknown protein	0	At2g33180	0.77
232	hypothetical protein	0	At1g66890	0.69
233		0	At1g74730	0.74
234	putative ribosomal protein S9	1E-122	At1g74970	0.70
235	phenylalanine ammonia-lyase	3E-51	At3g53260	0.53
236	unknown protein	2E-27	At1g78110	0.76
237	unknown protein	0	At1g18300	0.75
238	putative prolylcarboxypeptidase	1E-174	At2g24280	0.64
239	unknown protein	1E-12	At3g24100	0.76
240	unknown protein	0	At3g18990	0.39
241	hypothetical protein	1E-127	At1g78890	0.75
242	unknown protein	5E-87	At2g21530	0.71
243	hypothetical protein	1E-172	At1g20340	0.71
244	putative glucosyltransferase	0	At2g31790	0.63
245	allergen like protein	1E-129	At4g17030	0.74
246	unknown protein	0	At1g73750	0.72
247	APG5 (autophagy 5)-like protein	0	At5g17290	0.70

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248	putative protochlorophyllide reductase	0	At1g03630	0.57
249	zinc finger protein, putative	0	At3g19580	0.61
250	unknown protein	0	At2g35190	0.65
251	phosphate/triose-phosphate translocator precursor (gb|AAC83815.1)	4E-33	At5g46110	0.73
252	unknown protein	0	At5g50840	0.77
253	hypothetical protein	0	At4g34090	0.69
254	hypothetical protein	0	At1g14340	0.64
255	unknown protein	0	At1g67860	0.42
256	tyrosine transaminase like protein	1E-180	At4g23600	0.47
257		1E-173	At1g53890	0.53
258	pectinesterase, putative	0	At1g41830	0.76
259	putative protein	4E-72	At5g45550	0.69
260	putative ligand-gated ion channel subunit	2	At2g32400	0.45
261	unknown protein	0	At3g19370	0.42
262	putative protein	5E-13	At5g62580	0.59
263	putative protein	0	At3g61080	0.42
264	putative squamosa-promoter binding protein 2	1E-162	At1g27360	0.74
265	sucrose-phosphate synthase - like protein	0	At4g10120	0.22
266	hypothetical protein	4E-23	At1g62180	0.43
267	ribosomal protein	0	At4g15000	0.75
268	MYB-related transcription factor (CCA1)	0	At2g46830	0.46
269	pinoresinol-lariciresinol reductase, putative	1E-124	At1g32100	0.72
270	putative protein	0	At3g52230	0.71
271	3-keto-acyl-CoA thiolase 2 (gb|AAC17877.1)	0	At5g48880	0.57
272	putative protein	0	At3g46780	0.63
273	DNA-binding protein, putative	0	At1g01060	0.62
274	putative protein	3E-20	At4g30990	0.60
275	putative protein	0	At3g46780	0.59
276	hypothetical protein	1E-174	At1g28400	0.58
277	DNA binding protein - like	0	At5g61600	0.55
278	putative protein	0	At3g62260	0.72
279	putative CCCH-type zinc finger protein	0	At2g25900	0.63
280	ubiquitin-conjugating enzyme E2-17 kD 8 (ubiquitin-protein ligase	3E-16	At5g41700	0.42
281				0.64
282	microbody NAD-dependent malate dehydrogenase	0	At5g09660	0.63
283	glyceraldehyde 3-phosphate dehydrogenase A subunit (GapA)	0	At3g26650	0.63
284	microbody NAD-dependent malate dehydrogenase	0	At5g09660	0.66
285	sedoheptulose-bisphosphatase precursor	0	At3g55800	0.54
286	putative Fe(II) transporter	1E-175	At2g32270	0.74
287	germin - like protein	0	At5g38940	0.75
288	putative malonyl-CoA:Acyl carrier protein transacylase	0	At2g30200	0.70
289	hypothetical protein	0	At1g19000	0.61
290	FRO1-like protein; NADPH oxidase-like	0	At5g49740	0.41
291	J8-like protein	0	At1g80920	0.51
292	putative protein	0	At4g34190	0.63
293	photosystem II stability/assembly factor HCF136 (sp|O82660)	0	At5g23120	0.66
294	hypothetical protein	0	At4g24930	0.63
295	2-cys peroxiredoxin-like protein	0	At5g06290	0.69
296	putative protein	0	At3g53470	0.54

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297	unknown protein	3E-96	At3g02180	0.71
298	F12P19.7	0	At1g65900	0.69
299	putative fibrillin	0	At4g04020	0.28
300	putative protein	0.13	At4g18810	0.72
301	hypothetical protein	1E-171	At1g50240	0.67
302	putative protein	0	At3g63210	0.76
303	unknown protein	0	At2g32870	0.47
304	Glucose-1-phosphate adenylyltransferase (ApL1/adg2)	0	At5g19220	0.64
305	unknown protein	1E-66	At2g46100	0.67
306	farnesyl diphosphate synthase precursor (gb|AAB49290.1)	0	At5g47770	0.71
307	pyridoxine biosynthesis protein - like	0	At5g01410	0.47
308	hypothetical protein	0	At4g03820	0.71
309	putative myrosinase-binding protein	1E-47	At2g39310	0.38
310	unknown protein	0	At1g05870	0.44
311	heat shock protein, putative	0	At1g06460	0.28
312	RIBOSOMAL PROTEIN, putative	1E-175	At1g71720	0.76
313	elongation factor G, putative	0	At1g62750	0.65
314	mitochondrial Lon protease homolog 1 precursor (sp|O64948)	0	At5g47040	0.76
315	cytochrome c	2E-37	At4g10040	0.72
316	hypothetical protein	1E-102	At4g03420	0.69
317	putative DnaJ protein	1E-160	At2g41000	0.73
318	hypothetical protein	0	At2g27290	0.61
319	putative protein	1E-117	At5g50100	0.40
320	phytoene synthase (gb|AAB65697.1)	0	At5g17230	0.64
321	putative protein	0	At4g28230	0.73
322	hypothetical protein	0	At2g01260	0.49
323	unknown protein	0	At3g17520	0.71
324	Ran binding protein (AtRanBP1b)	0	At2g30060	0.73
325	putative protein	0	At4g32190	0.63
326	unknown protein	0	At1g19400	0.64
327	sucrose-phosphate synthase-like protein	0	At5g20280	0.67
328	putative protein	1E-136	At5g03545	0.45
329	biotin carboxyl carrier protein precursor-like protein	1E-124	At5g15530	0.54
330	unknown protein	4E-85	At1g16320	0.53
331	unknown protein	5E-16	At3g32930	0.68
332	putative protein	1E-142	At4g35290	0.74
333	glutathione S-transferase-like protein	0	At5g17220	0.66
334	fructose 1,6-bisphosphatase, putative	0	At1g43670	0.63
335	peptidylprolyl isomerase-like protein	2E-34	At5g13120	0.72
336	teosinte branched1 - like protein	0	At4g18390	0.63
337	putative protein	0	At3g51520	0.71
338	lactoylglutathione lyase-like protein	0	At1g11840	0.45
339	late embryogenesis abundant protein LEA like	0	At5g06760	0.55
340	putative protein	1E-177	At5g19590	0.71
341	putative protein	0	At3g63190	0.72
342	hypothetical protein	0	At1g69510	0.47
343	putative protein kinase	0	At2g30040	0.69
344	xyloglucan endo-transglycosylase	0	At3g44990	0.43
345	phospholipid hydroperoxide glutathione peroxidase	0	At4g11600	0.71
346	sedoheptulose-bisphosphatase precursor	0	At3g55800	0.51
347	Clp proteinase like protein	2E-55	At4g17040	0.75

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348	unknown protein	0	At5g07020	0.68
349	unknown protein	2E-32	At5g51720	0.49
350	endomembrane protein, putative	1E-117	At1g14670	0.75
351	putative phosphomannomutase	0	At2g45790	0.66
352	putative protein	1E-95	At4g27280	0.46
353	mrp protein, putative	0	At3g24430	0.75
354	putative vacuolar ATPase	0	At4g02620	0.74
355	phosphate transporter, putative	0	At3g26570	0.61
356	similar to Trp Asp repeat protein emb|CAB39845.1; similar to EST	0	At1g78070	0.74
357	putative MAP kinase	2E-18	At2g01450	0.51
358	ethylene-responsive transcriptional coactivator, putative	0	At3g24500	0.51
359	6-phosphogluconolactonase-like protein	0	At5g24420	0.52
360	beta-amylase-like proten	1E-175	At5g18670	0.40
361	hypothetical protein	3E-53	At1g20970	0.72
362	chloroplast 50S ribosomal protein L31, putative	0	At1g75350	0.74
363	cytochrome P450-like protein	0	At4g37320	0.67
364	putative potassium transporter AtKT5p (AtKT5)	0	At4g33530	0.76
365	putative ribosomal-protein S6 kinase (ATPK6)	0	At3g08730	0.63
366	hypothetical protein	0	At1g04770	0.68
367	transcription factor Hap5a	6E-74	At3g48590	0.60
368	putative protein	0	At5g20070	0.69
369	beta-expansin	0	At2g20750	0.72
370	SOUL-like protein	4E-82	At1g17100	0.71
371	unknown protein	0	At1g70760	0.40
372	unknown protein	1E-124	At2g20890	0.73
373	unknown protein	1E-160	At1g07280	0.72
374	unknown protein	0	At1g64680	0.65
375	ADPG pyrophosphorylase small subunit (gb|AAC39441.1)	0	At5g48300	0.68
376	unknown protein	0	At2g17340	0.61
377	hypothetical protein	0	At1g26800	0.74
378	unknown protein	0	At1g22930	0.67
379	polyphosphoinositide binding protein, putative	0	At1g01630	0.72
380	caffeoyl-CoA O-methyltransferase - like protein	0	At4g34050	0.67
381	pectinesterase	0	At5g53370	0.56
382	unknown protein	7E-75	At1g64370	0.43
383	p-nitrophenylphosphatase-like protein	0	At5g36790	0.52
384	putative protein	1E-172	At5g55960	0.64
385	serine/threonine protein kinase -like protein	0	At5g10930	0.26
386	cytosolic factor, putative	0	At1g72160	0.67
387	S-adenosylmethionine:2-demethylmenaquinone methyltransferase-like	1E-159	At5g56260	0.76
388	pectate lyase	0	At5g63180	0.67
389	vacuolar sorting receptor-like protein	0	At4g20110	0.70
390	putative membrane channel protein	0	At2g28900	0.76
391	putative thylakoid lumen rotamase	0	At3g01480	0.56
392	putative chloroplast prephenate dehydratase	0	At3g44720	0.73
393	3-oxoacyl-[acyl-carrier-protein] synthase I precursor	0	At5g46290	0.76
394	P-Protein - like protein	1E-108	At4g33010	0.73
395	NHE1 Na+/H+ exchanger	1E-122	At5g27150	0.73
396	receptor kinase-like protein	0	At3g47580	0.72
397	raffinose synthase -like protein	0	At5g40390	0.59

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398		0	At1g54780	0.63
399	unknown protein	0	At2g46170	0.73
400	beta-xylan endohydrolase -like protein	0.085	At4g33810	0.26
401	putative protein	1E-137	At4g12700	0.60
402	putative ribose 5-phosphate isomerase	0	At3g04790	0.76
403	putative protein	0	At5g47840	0.70
404	putative RNA-binding protein	0	At1g09340	0.57
405	adenine phosphoribosyltransferase (EC 2.4.2.7) - like protein	0	At4g22570	0.46
406	unknown protein	0	At3g15950	0.37
407	putative glutathione peroxidase	7E-12	At2g25080	0.46
408	putative protein	0	At5g23060	0.63
409	pectate lyase 1-like protein	0	At1g67750	0.42
410	putative triosephosphate isomerase	9E-61	At2g21170	0.66
411	carbonate dehydratase - like protein	0	At4g33580	0.72
412	putative protein	0	At5g37300	0.56
413	putative protein	1E-143	At3g60080	0.77
414	cystatin (emb|CAA03929.1)	2E-83	At5g12140	0.74
415	putative cytochrome b5	0	At2g46650	0.46
416	putaive DNA-binding protein	0.00000002	At4g31550	0.63
417	hypothetical protein	1E-143	At3g21050	0.50
418	putative beta-hydroxyacyl-ACP dehydratase	0	At2g22230	0.59
419	2-oxoglutarate/malate translocator	0	At5g64290	0.77
420	hypothetical protein	1E-123	At3g27050	0.49
421	putative alcohol dehydrogenase	9E-64	At2g37770	0.64
422	hypothetical protein	1E-107	At1g18730	0.67
423	putative pectinacetylesterase	0	At4g19420	0.71
424	similar to ADP-ribosylation factor gb|AAD17207; similar to ESTs	2E-80	At1g10630	0.67
425	hypothetical protein	0	At1g04420	0.67
426	putative protein	0	At4g26710	0.62
427	putative protein	0	At4g34630	0.72
428		0	At1g70890	0.29
429	RCc3- like protein	0	At4g22490	0.57
430	hypothetical protein	5E-53	At1g20450	0.49
431	glucosyltransferase-like protein	3E-31	At5g22740	0.65
432	glutathione S-transferase	0	At2g29450	0.52
433	putative protein	0	At3g44450	0.59
434	cysteine synthase	0	At5g28020	0.60
435		0	At4g04640	0.57
436	40S ribosomal protein S14	1E-25	At2g36160	0.67
437	putative protein	0	At4g19100	0.76
438	K Efflux antiporter KEA1	0	At1g01790	0.65
439	hypothetical protein	1E-169	At2g42980	0.66
440	cytochrome P450 like protein	0.11	At4g36380	0.48
441	unknown protein	8E-64	At2g01520	0.23
442	hypothetical protein	1E-157	At1g07130	0.66
443	putative protein	0.0005	At5g09620	0.62
444	unknown protein	0	At1g08470	0.66
445	putative protein	6E-37	At3g54600	0.70
446	DnaJ - like protein	1E-68	At4g39960	0.52
447	putative protein phosphatase 2C	1E-161	At1g78200	0.72

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448	biotin synthase (Bio B)	0	At2g43360	0.67
449	unknown protein	3E-69	At3g17510	0.55
450	high mobility group protein 2-like	1E-107	At3g51880	0.66
451	putative proline-rich protein	0	At2g21140	0.57
452	cyclin delta-3	0	At4g34160	0.74
453	SERINE CARBOXYPEPTIDASE II - like protein	0	At4g30810	0.77
454	unknown protein	0	At1g67330	0.70
455	putative protein	7E-93	At3g56010	0.70
456	GTP-binding protein LepA homolog	0	At5g08650	0.76
457	unknown protein	0	At3g10420	0.42
458	putative protein	0	At3g51510	0.58
459	putative protein	0	At3g45870	0.73
460	putative enolase	0	At1g74030	0.65
461	putative protein	0.00003	At5g11680	0.71
462	putative protein	0	At5g26280	0.58
463	O-methyltransferase, putative	0	At1g21100	0.63
464	beta-1,3-glucanase class I precursor	0	At4g16260	0.51
465	protein phosphatase 2C (PP2C)	2E-27	At3g11410	0.67
466	root cap protein 2-like protein	1E-174	At5g54370	0.75
467	putative adenosine phosphosulfate kinase	0	At2g14750	0.47
468	putative protein	0	At4g30010	0.73
469	putative uroporphyrinogen decarboxylase	0.000000002	At2g40490	0.75
470	putative protein	1E-151	At3g57400	0.71
471	branched-chain amino acid aminotransferase, putative	1E-56	At3g19710	0.30
472	copia-like retroelement pol polyprotein	0	At2g19830	0.72
473	neoxanthin cleavage enzyme-like protein	0	At4g19170	0.38
474	hypothetical protein	0	At1g31860	0.70
475	unknown protein	0	At2g26570	0.61
476	asparagine synthetase ASN3	0	At5g10240	0.72
477	hypothetical protein	1E-80	At1g64770	0.56
478	expansin S2 precursor, putative	1E-114	At1g20190	0.51
479	5'-adenylylsulfate reductase	0	At4g04610	0.43
480	putative protein	0.088	At3g59680	0.71
481	putative MYB family transcription factor	4E-31	At2g37630	0.73
482	Putative protein kinase	3E-23	At1g51850	0.60
483	putative protein	0	At5g15910	0.76
484	AALP protein	0	At5g60360	0.63
485	putative galactinol synthase	0	At2g47180	0.69
486	cyanohydrin lyase like protein	0	At4g16690	0.56
487	putative protein	0	At5g03880	0.57
488	putative glucosyltransferase	0	At2g30150	0.73
489	cysteine endopeptidase precursor - like protein	0	At3g48350	0.65
490	unknown protein	1E-122	At3g07700	0.70
491	putative peroxiredoxin	2E-86	At3g26060	0.76
492		0	At1g73500	0.58
493	hypothetical protein	7E-74	At1g64780	0.52
494	UDP glucose:flavonoid 3-o-glucosyltransferase, putative	2E-90	At1g30530	0.59
495	hypothetical protein	0	At4g02800	0.55
496	oxidoreductase -like protein	0	At3g55290	0.65
497	hypothetical protein	0	At1g50670	0.73
498	carnitine/acylcarnitine translocase-like protein	0	At5g46800	0.58
499		1E-169	At4g00780	0.57

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500		0	At1g22630	0.76
501	cytochrome P450-like protein	0	At4g37330	0.72
502	putative endo-1,4-beta glucanase	8E-36	At4g02290	0.62
503	hevein-like protein precursor	0	At3g04720	0.75
504	leucine zipper-containing protein AT103	1E-139	At3g56940	0.63
505	delta-1-pyrroline-5-carboxylate synthetase	0	At3g55610	0.69
506	remorin	0	At2g45820	0.76
507	putative protein	0	At5g22460	0.48
508	putative lectin	0	At3g16530	0.43
509	putative protein	9E-29	At5g26260	0.52
510	peptidylprolyl isomerase ROC4	0	At3g62030	0.61
511	O-methyltransferase, putative	0	At1g21130	0.63
512	putative zinc finger protein	0	At4g38960	0.72
513	putative hydroxyproline-rich glycoprotein	1E-173	At1g13930	0.58
514	putative protein 1 photosystem II oxygen-evolving complex	0	At3g50820	0.65
515	hypothetical protein	0	At1g66700	0.63
516	unknown protein	0	At1g52870	0.43
517	heat shock protein 90	0	At5g56010	0.75
518	Overlap with bases 87,142-90,425 of 'IGF' BAC clone F9K20, accession	1E-115	At1g78570	0.63
519	phosphoglycerate kinase, putative	1E-120	At3g12780	0.73
520	putative lectin	1E-25	At3g16400	0.40
521	profilin 2	0	At4g29350	0.77
522	HSP associated protein like	5E-16	At4g22670	0.75
523	putative cell division control protein, cdc2 kinase	1E-75	At1g20930	0.72
524	putative protein	1E-107	At5g08050	0.65
525	ribosomal protein S27	0	At5g47930	0.77
526	vacuolar H+-transporting ATPase 16K chain	0	At4g34720	0.76
527	expansin At-EXP5	3E-82	At3g29030	0.52
528	similar to cold acclimation protein WCOR413 [Triticum aestivum]	0	At2g15970	0.74
529	chloroplast membrane protein (ALBINO3)	1E-159	At2g28800	0.72
530	putative thioredoxin	1E-102	At1g08570	0.55
531	unknown protein	0	At1g08380	0.65
532	hypothetical protein	0	At1g07180	0.53
533	putative flavonol sulfotransferase	0	At1g74090	0.69
534	possible apospory-associated like protein	0	At4g25900	0.71
535	glycolate oxidase, putative	0	At3g14420	0.71
536	putative peroxidase ATP2a	0	At2g37130	0.75
537	putative protein	1E-154	At4g21860	0.75
538	hydroxypyruvate reductase (HPR)	0	At1g68010	0.74
539	photosystem I reaction centre subunit psaN precursor (PSI-N)	0	At5g64040	0.49
540	plastid ribosomal protein S6, putative	0	At1g64510	0.60
541	methylenetetrahydrofolate reductase MTHFR1	0	At3g59970	0.72
542	putative photosystem I reaction center subunit II precursor	0	At1g03130	0.55
543	unknown protein	0	At3g10940	0.64
544	fumarate hydratase	0	At5g50950	0.43
545	Lil3 protein	0	At5g47110	0.73
546	homeobox gene ATH1	0	At4g32980	0.76
547	putative lectin	3E-20	At3g16390	0.43
548	COP1-interacting protein 7 (CIP7)	0.0000001	At4g27430	0.67

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549	putative acyl-CoA synthetase	0	At2g47240	0.51
550	unknown protein	0	At2g01590	0.68
551	hydroxymethyltransferase	0	At4g13930	0.72
552	hypothetical protein	1E-164	At1g69490	0.27
553	SNF1 related protein kinase (ATSRPK1)	1E-170	At3g23000	0.49
554	mevalonate diphosphate decarboxylase	6E-68	At2g38700	0.71
555	putative flavonol sulfotransferase	0	At1g74090	0.69
556	protein phosphatase 2C (AtP2C-HA)	0	At1g72770	0.59
557	cinnamoyl-CoA reductase - like protein	0	At4g30470	0.72
558	O-methyltransferase - like protein	0	At4g35160	0.50
559	pyruvate dehydrogenase E1 alpha subunit	0	At1g01090	0.77
560	putative chlorophyll A-B binding protein	0	At3g27690	0.49
561	putative UDP-N-acetylglucosamine pyrophosphorylase	0	At2g35020	0.69
562	putative protein	1E-121	At4g05590	0.75
563	Ca2+-dependent membrane-binding protein annexin	0	At1g35720	0.41
564	hypothetical protein	0	At2g35760	0.51
565	hypothetical protein	2E-15	At1g18840	0.71
566	hypothetical protein	0	At1g51140	0.53
567	aromatic amino-acid decarboxylase - like protein	0	At4g28680	0.73
568	unknown protein	3E-72	At2g35830	0.49
569	hypothetical protein	0	At1g78690	0.66
570	putative elongation factor P (EF-P)	0	At3g08740	0.74
571	unknown protein	0	At1g22750	0.76
572	putative protein	0	At3g63160	0.45
573	unknown protein	1E-150	At3g26510	0.55
574	aldo/keto reductase-like protein	0	At5g53580	0.69
575	glycine decarboxylase complex H-protein	0	At2g35370	0.53
576	thioredoxin (clone GIF1) (pir||S58118)	3E-14	At5g42980	0.53
577	putative protein	1E-93	At4g28020	0.52
578	hypothetical protein	0	At1g18870	0.71
579	vegetative storage protein Vsp2	0	At5g24770	0.43
580	putative protein	3E-75	At4g17560	0.66
581	NBD-like protein (gb|AAD20643.1)	0	At5g44110	0.58
582	photosystem I subunit V precursor, putative	1E-119	At1g55670	0.56
583	putative thaumatin	2E-36	At2g28790	0.64
584	hyoscyamine 6-dioxygenase hydroxylase, putative	0	At1g35190	0.71
585	H-protein promoter binding factor-like protein	0	At5g62430	0.51
586	putative protein	0	At4g04840	0.52
587	endo-xyloglucan transferase - like protein	0	At4g37800	0.68
588	putative protein	0	At4g26850	0.33
589	hypothetical protein	0	At3g12340	0.69
590	putative acetone-cyanohydrin lyase	0	At2g23610	0.68
591	putative transcription factor	0	At1g71030	0.36
592	hypothetical protein	1E-128	At1g19000	0.74
593	putative xyloglucan endo-transglycosylase	7E-27	At2g36870	0.40
594	hypothetical protein	3E-51	At1g58080	0.77
595	putative protein	1E-167	At5g36800	0.65
596	putative protein	1E-157	At4g30530	0.65
597	cinnamyl-alcohol dehydrogenase ELI3-1	0	At4g37980	0.54
598	putative CONSTANS-like B-box zinc finger protein	0	At2g47890	0.72
599	unknown protein	1E-123	At1g53480	0.60
600	protein phosphatase 2C-like protein	2E-55	At4g28400	0.72

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601	putative protein	0	At5g60680	0.57
602	farnesyl-pyrophosphate synthetase FPS2	0	At4g17190	0.76
603	soluble inorganic pyrophosphatase, putative	0	At1g01050	0.59
604	putative nematode-resistance protein	1E-117	At2g40000	0.34
605	putative AP2 domain transcription factor	0	At2g23340	0.74
606	putative myo-inositol monophosphatase	3E-17	At3g02870	0.60
607	putative isoamylase	0	At1g03310	0.74
608	phosphate transporter (AtPT2)	0	At2g38940	0.76
609	putative disease resistance response protein	0	At4g11190	0.68
610	unknown protein	0	At2g45600	0.55
611	peroxidase ATP13a	0	At5g17820	0.70
612	unknown protein	0	At1g26920	0.74
613	putative mitochondrial carrier protein	0	At2g47490	0.69
614	actin depolymerizing factor 3 - like protein	1E-136	At5g59880	0.64
615	putative protein transport protein SEC23	1E-149	At2g21630	0.73
616	unknown protein	2E-30	At2g44310	0.74
617	putative protein	0	At4g21570	0.69
618	putative steroid binding protein	0	At2g24940	0.57
619	putative lipid transfer protein	0	At2g15050	0.49
620	hypothetical protein	0	At4g15510	0.75
621	unknown protein	3E-47	At3g25690	0.56
622	40S ribosomal protein S19 - like	0	At5g28060	0.73
623	putative auxin-regulated protein	0	At2g21210	0.56
624	unknown protein	0	At1g19350	0.71
625	unknown protein	1E-136	At1g07700	0.71
626	50S ribosomal protein L27	0	At5g40950	0.70
627	unknown protein	1E-105	At2g46540	0.69
628	ATP-sulfurylase	0	At4g14680	0.72
629	hypothetical protein	1E-107	At3g18890	0.64
630	putative protein	0	At3g59780	0.62
631	cytochrome P450 monooxygenase - like protein	0	At4g37410	0.56
632	hypothetical protein	2E-86	At1g61890	0.36
633	ubiquitin-conjugating enzyme, putative	0	At3g20060	0.66
634	hypothetical protein	0	At1g20810	0.74
635	hypothetical protein	0	At2g15020	0.45
636	unknown protein	0	At1g55480	0.52
637	UDP glucose:flavonoid 3-o-glucosyltransferase -like protein	0	At5g17050	0.56
638	hypothetical protein	0	At3g23670	0.69
639	putative protein	0	At4g34920	0.69
640	unknown protein	1E-100	At2g36630	0.71
641	unknown protein	6E-94	At1g56580	0.63
642	HSR201 like protein	0	At4g15390	0.75
643	heme oxygenase 1 (HO1)	0	At2g26670	0.74
644	putative beta-glucosidase	0	At4g27820	0.46
645	unknown protein	1E-122	At1g68440	0.45
646	predicted protein	0	At4g22820	0.54
647	putative kinesin heavy chain	0	At2g22610	0.72
648	putative protein	0	At4g27860	0.61
649	unknown protein	0	At2g37240	0.76
650	unknown protein	0	At1g30070	0.76
651	WD-repeat protein -like protein	0	At4g33270	0.57
652	unknown protein	0	At1g32220	0.60

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653	hypothetical protein	0	At4g22920	0.73
654	putative amino acid transporter protein	0	At3g11900	0.67
655	endo-beta-1,4-glucanase, putative	0	At1g64390	0.50
656	hypothetical protein	0	At1g18060	0.60
657	hypothetical protein	1E-114	At4g39820	0.70
658	putative protein	1E-62	At5g27290	0.60
659	putative protein	1E-133	At3g48200	0.46
660	hypothetical protein	1E-173	At1g64500	0.51
661	putative ribonuclease, RNS2	0	At2g39780	0.60
662	thioredoxin f1	0	At3g02730	0.59
663	unknown protein	0	At2g20670	0.67
664	cytochrome P450-like protein	0	At5g48000	0.45
665	subtilisin proteinase - like	1E-105	At4g21650	0.31
666	photoassimilate-responsive protein PAR-1b -like protein	0	At3g54040	0.76
667	putative dTDP-glucose 4-6-dehydratase	0	At2g27860	0.45
668	hypothetical protein	0	At1g51700	0.43
669	early light-induced protein	0	At3g22840	0.65
670	hypothetical protein	0	At1g32060	0.42
671	unknown protein	0	At2g34860	0.69
672	peroxidase ATP3a (emb|CAA67340.1)	4E-10	At5g64100	0.49
673	putative protein	0	At5g06770	0.67
674	hypothetical protein	0	At2g16860	0.57
675	annexin	0	At5g65020	0.61
676	thioredoxin, putative	0	At1g50320	0.63
677	putative protein	0	At5g17360	0.66
678	nucleoside diphosphate kinase 3 (ndpk3)	0	At4g11010	0.76
679	unknown protein	0	At5g62550	0.64
680	putative protein	0	At4g12000	0.62
681	cell division protease FtsH, putative	0	At1g06430	0.65
682	unknown protein	0	At1g74880	0.41
683	putative protein	0	At5g56540	0.61
684	unknown protein	0	At1g68780	0.61
685	mipC protein - like (aquaporin)	0	At5g60660	0.64
686	Oxygen-evolving enhancer protein 3 precursor - like protein	0	At4g05180	0.64
687	cytochrome P450, putative	0	At3g26180	0.74
688	putative protein	1E-126	At5g22210	0.74

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CLAIMS

1. A method to alter plant characteristics comprising modulating, in a plant, the expression of one or more nucleic acids and/or modulating the activity of one or more proteins, said nucleic acids or proteins being essentially similar to any one of SEQ ID NO 1 to 104 and/or being essentially similar to a nucleic acid sequence or protein sequence deposited under accession number At1g57680 and/or deposited under any of the accession numbers presented in Tables 1, 2, 4 or 5.

2. A method according to claim 1, wherein said modified plant characteristic is selected from any one or more of the following: altered development, increased yield and/or biomass, altered plant architecture, altered plant biochemistry, altered plant physiology, altered metabolism, enhanced survival capacity and/or enhanced stress tolerance, each relative to corresponding wild type plants.

3. A method according to claim 2, wherein said altered metabolism comprises altered nitrogen and/or carbon metabolism.

4. A method according to claims 1, wherein said altered characteristic comprises altered DNA synthesis and/or altered endoreduplication and/or altered storage lipid mobilization and/or altered photosynthesis.

5. A recombinant nucleic acid comprising:
(a) one or more nucleic acid sequences essentially similar to any one of SEQ ID NO 1 to 52 and/or being essentially similar to a nucleic acid sequence deposited under accession number At1g57680 and/or deposited under any of the accession numbers presented in Tables 4 or 5, or the complement thereof; and optionally operably linked to
(b) a regulatory sequence

6. A recombinant nucleic acid according to claim 5, wherein said regulatory sequence is a plant-expressible promoter.

7. A method for making a transgenic plant, comprising introduction of a recombinant nucleic acid according to claim 5 or 6 into a plant.

8. A method according to claim 7, comprising stably integrating into the genome of a plant a recombinant nucleic acid according to claim 5.

9. A method according to any of claims 1 to 4 or 7 to 8, comprising overexpression of one or more nucleic acids essentially similar to any one of SEQ ID NO 1 to 52 and/oror being essentially similar to a nucleic acid deposited under accession number At1g57680 and/or deposited under any of the accession numbers presented in Tables 4 or 5, and/or wherein said method comprises enhancing the activity of one or more proteins essentially similar to any one of SEQ ID NO 53 to 104 and/or being essentially similar a protein sequence deposited under accession number At1g57680 and/or deposited under any of the accession numbers presented in Tables 1, 2, 4 or 5.

10. A method according to any of claims 1 to 4 or 7 to 8, comprising downregulation of expression of one or more nucleic acids essentially similar to any one of SEQ ID NO 1 to 52 and/or being essentially similar to a nucleic acid deposited under accession number At1g57680 and/or deposited under any of the accession numbers presented in Tables 4 or 5, and/or wherein said method comprises decreasing the activity of one or more proteins essentially similar to SEQ ID NO 53 to 104 or being essentially similar to a protein sequence deposited under accession number At1g57680 and/or deposited under any of the accession numbers presented in Tables 4 or 5.

11. A transgenic plant obtainable by a method according to any of claims 1 to 4 or 7 to 10.

12. A transgenic plant comprising a recombinant nucleic acid sequence essentially similar to any one of SEQ ID NO 1 to 104 and/or being essentially similar to a nucleic acid sequence deposited under accession number At1g57680 and/or deposited under any of the accession numbers presented in Tables 1, 2, 4 or 5, or the complement thereof.

13. An ancestor, progeny, or any plant part, particularly a harvestable part, of a transgenic plant of claim 11 or 12.

14. Use of a nucleic acid sequence encoding a protein essentially similar to any one of SEQ ID NO 53 to 104 or being essentially similar to the protein sequence deposited under accession number At1g57680 and/or deposited under any of the accession numbers presented in Tables 1, 2, 4 or 5, or a homologue, a derivative or functional fragment thereof for altering growth characteristics in a plant.

15. Use of a protein essentially similar to any one of SEQ ID NO 53 to 104 or being essentially similar to the nucleic acid sequence deposited under the accession number At1g57680 or deposited under any of the accession numbers presented in Tables 1, 2, 4 or 5, or a homologue, a derivative or functional fragment thereof, for altering plant characteristics.

16. Use of a nucleic acid sequence essentially similar to any one of SEQ ID NO 1 to 52 and/or being essentially similar to the nucleic acid sequence deposited under accession number At1g57680 and/or deposited under any of the accession numbers presented in Tables 1, 2, 4 or 5, or a homologue, a derivative or functional fragment thereof, for marker assisted breeding of plants with altered characteristics.

17. Use of a nucleic acid sequence essentially similar to any one of SEQ ID NO 1 to 52 and/or being essentially similar to the nucleic acid sequence deposited under accession number At1g57680 and/or deposited under any of the accession numbers presented in Tables 1, 2, 4 or 5, or a homologue, a derivative or functional fragment thereof, for conventional breeding of plants with altered characteristics.

18. Use of a nucleic acid or a protein essentially similar to any one of SEQ ID NO 1 to 104 or a nucleic acid or protein being essentially similar to the nucleic acid or the protein sequence deposited under the accession number At1g57680 or deposited under any of the accession numbers presented in Tables 1, 2, 4 or 5, or a homologue, a derivative or functional fragment thereof, as a growth regulator.

19. A nucleic acid or a protein essentially similar to any one of SEQ ID NO 1 to 104 or a nucleic acid or protein being essentially similar to the nucleic acid or the protein sequence deposited under the accession number At1g57680 or deposited under any of the accession numbers presented in Tables 1, 2, 4 or 5, or a homologue, a derivative or functional fragment thereof, for use as a therapeutic agent

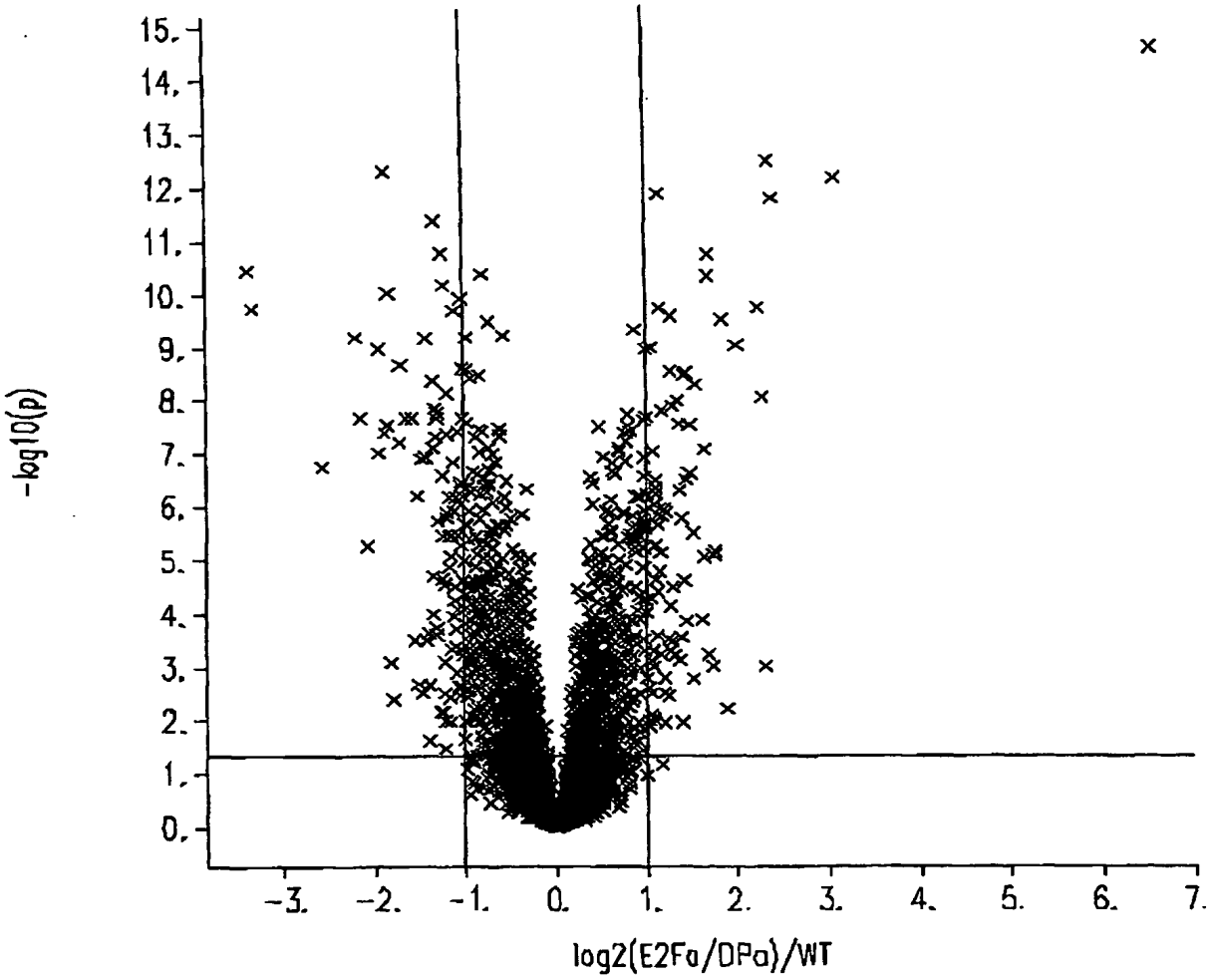
20. An isolated nucleic acid comprising one or more of the regulatory elements upstream of the startcodon of the nucleic acids represented by SEQ ID NO 1 to 104 and/or the nucleic acid deposited under accession number At1g57680 and/or deposited under any of the accession numbers presented in Tables 1, 2, 4 or 5.

21. An isolated nucleic acid according to claim 18, wherein said regulatory element is the natural promoter of said genes.

ABSTRACT

IDENTIFICATION OF NOVEL E2F TARGET GENES AND USE THEREOF

The present invention concerns a method for altering plant growth characteristics of a plant. The invention describes the identification of genes that are upregulated or downregulated in transgenic plants overexpressing E2Fa-Dpa and the use of such sequences to alter plant growth characteristics. A preferred way for altering growth characteristics of plant is to introduce into said plant a nucleic acid sequence upregulated or downregulated in plants overexpressing E2Fa/Dpa, or the complement thereof, or a homologue, derivative or active fragment thereof. Some of the genes identified in the present invention have an E2Fa target consensus sequence in their 5' upstream region. The identified genes play a role in a variety of biological processes, such as DNA replication, cell wall biosynthesis, nitrogen and/or carbon metabolism, transcription factors etc...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log2(E2Fa/DPa)/WT

FIGURE 1

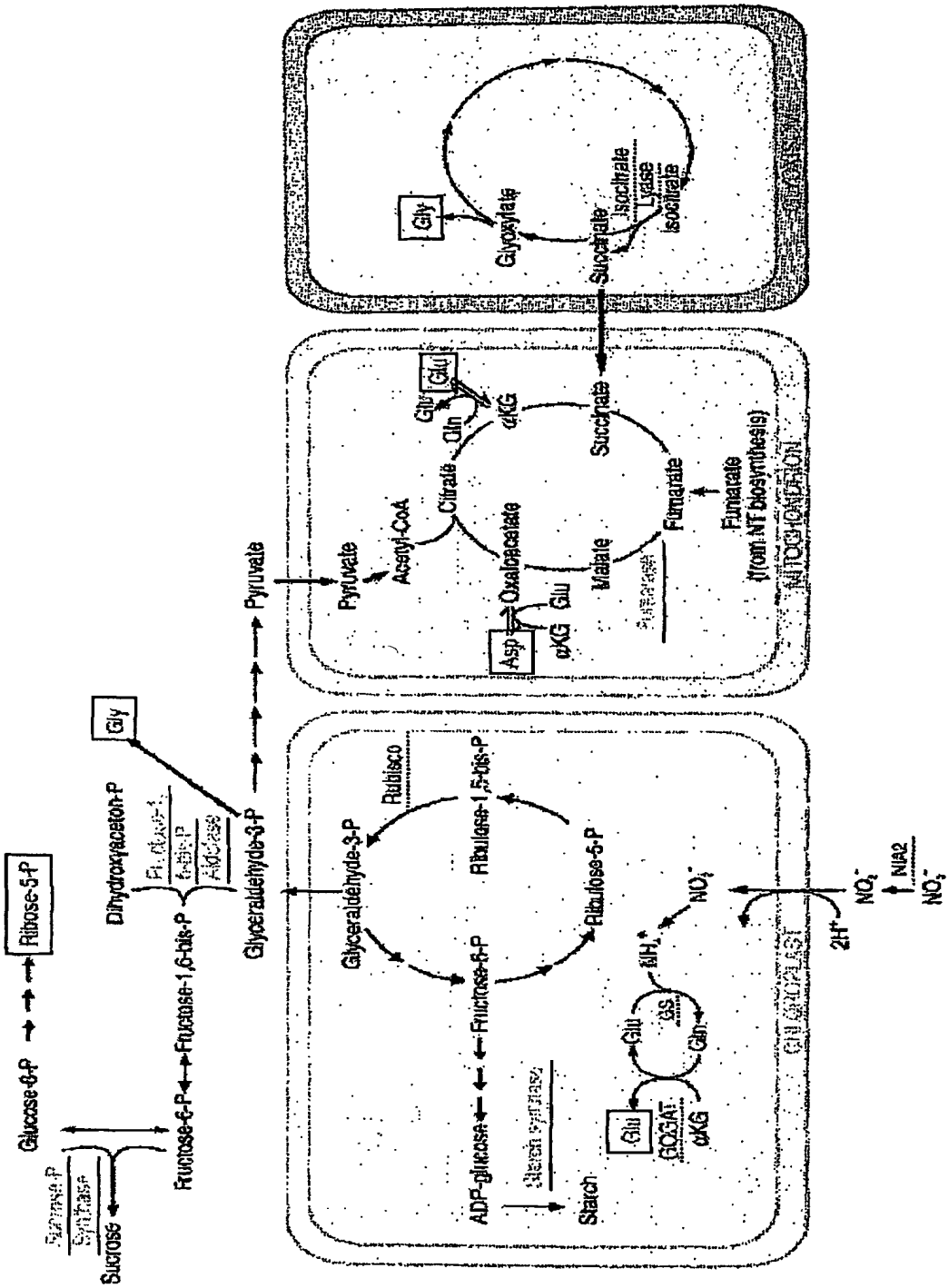
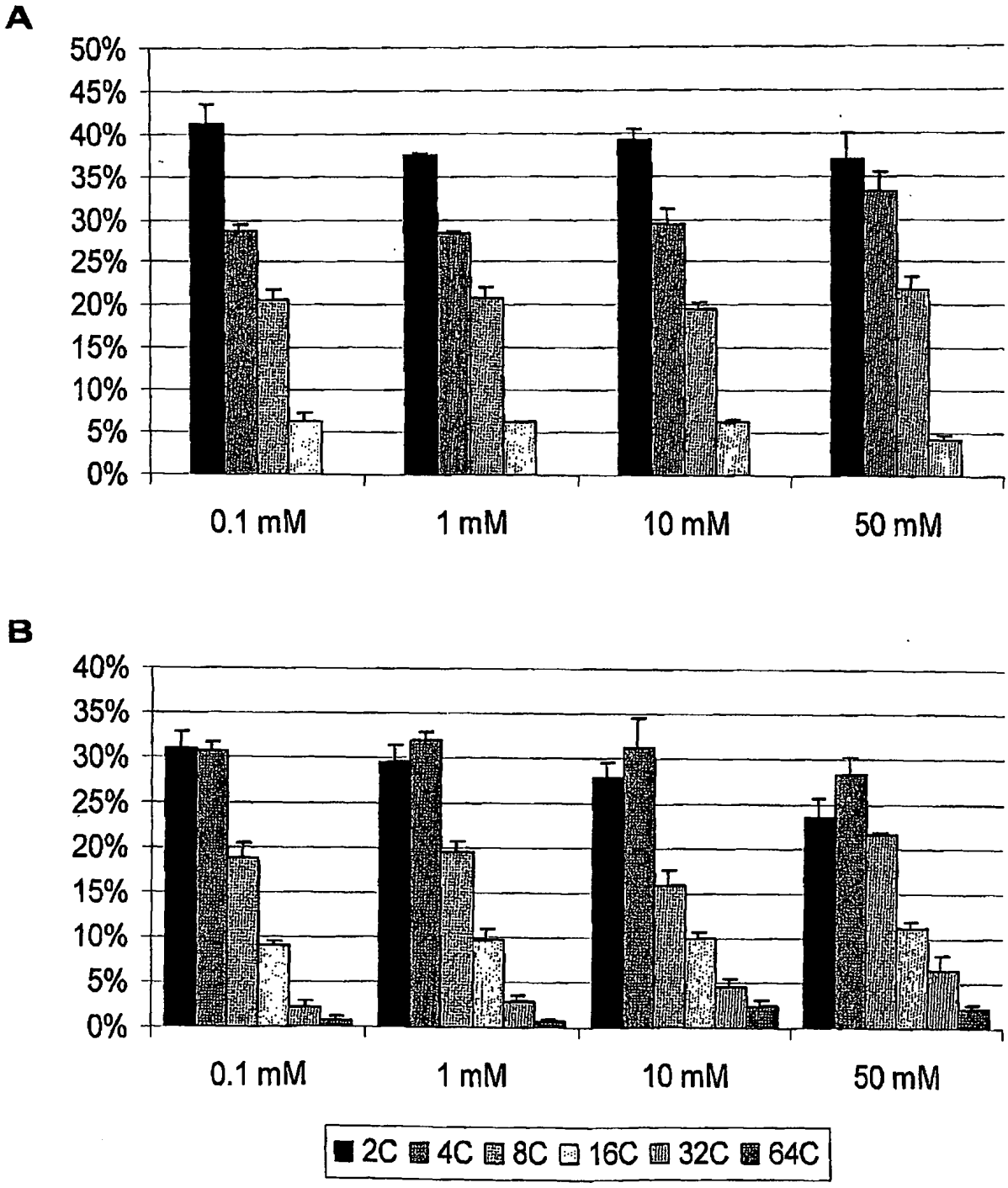

Ribose-5-P
Glucose-6-P
Fructose-6-P
Fructose-1,6-bis-P
Dihydroxyacetone-P
Glyceraldehyde-3-P
Gly
Pyruvate
Sucrose
Rubisco
Ribulose-1,5-bis-P
Ribulose-5-P
ADP-glucose
Starch
Fructose-6-P
Glu
GS
Gln
GOGAT
αKG
NO_3^-
NH_4^+
$2H^+$
NIA2
Pyruvate
Acetyl-CoA
Citrate
Oxaloacetate
Malate
Fumarate
Succinate
Asp
Glyoxylate
Isocitrate
Lyase isocitrate
Fumarate (from NT biosynthesis)
MITOCHONDRION
CHLOROPLAST

FIGURE 2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2C 4C 8C 16C 32C 64C

FIGURE 3

MATDB - entry At1g57680 from contig t8l23
(Chromosome 1 / BAC clone T8L23 / sequence database accession EMBL:AC079733) mips

Type: gene/protein
Code: At1g57680
Old code: T8L23_15
Title: putative protein
Contig: t8l23
Position: 53392-54480 (C)

Notes

•

Classification

- known protein

Functional Category

- UNCLASSIFIED PROTEINS

TargetP prediction

- Targeted to secretory pathway
- TargetP score: 0.968
- TargetP reliability class: 2
- Probable signal sequence length: -

TMHMM transmembrane prediction

- Very likely to be a transmembrane protein (or have a signal peptide) (Exp number of AA in TMHs: 110)
- A transmembrane region could actually be a signal peptide (Exp number, first 60 AAs: 21)
- Orientation of N-terminal: external side (probability: 0.9)
- Transmembrane regions:
  - 40-62
  - 83-100
  - 138-160
  - 181-203
  - 213-235

EMBL

- AY072149

mRNA matches: 1 found

Arabidopsis ESTs

- found **10**
  AA585779; AI992654; AI998042; AV518701; AV538415; AV538372; AV541088; AV550688; AV550640; AV554579;

FIGURE 4

Full report

- Full report includes FST matches and external annotation... slow.

Protein properties

PEDANT and Interpro data are being recalculated. To access old PEDANT data, use the link in the left frame, but be aware that some protein sequences have been changed due to update of gene models based on cDNA data and PEDANT data may be outdated.

Click here to submit new information about this entry

FIGURE 4 (contin.)

***A. thaliana* - contig t8l23 - entry At1g57680** mips

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LRAPLKMESG ALSGKWNRDT AGYIILYCLP MLALQLAVVL SESRLNGGSG SYVKLPHDFT
RTYSRVIIDH DEVALCTYPL LSTILLGVFA AVLTAYLFWL GRQILKLVIN KRLQKRVYTL
IFSVSSFLPL RIVMLCLSVL TAADKIIFEA LSFLAFLSLF CFCVVSICLL VYFPVSDSMA
LRGLRDTDDE DTAVTEERSG ALLLAPNSSQ TDEGLSLRGR RDSGGSTQER YVELSLFLEA
EN*
C; Length 362 aa
C; Sequence At1g57680 was extracted from t8l23
C; Fragment (54480-53392(C))
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FIGURE 4 (contin.)

047-E2F-PROV

***A. thaliana* - contig t8l23 - coordinates: 53392-54480 (C)** mips

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 121 CGTAAGCAAG GCTATATTCA ACTTGGTTAC TTCAGTGGTC CCTGGATTAT CCGAATCACT
 181 TTCATTCTCT TTGCTATCTG GTGGGCTGTT GGTGAGATTT TTCGATTGAG TTTGTTGAGG
 241 CGTCACAGAA GGTTGTTGAG TGGGTTGGAT CTGAGATGGC AAGAAAACGT TTGCAAGTGG
 301 TACATCGTTT CCAATCTAGG ATTTGCGGAG CCTTGTCTCT TTCTGACTCT CATGTTTCTT
 361 CTGCGTGCTC CCTTGAAGAT GGAATCAGGG GCTTTGAGCG GAAAATGGAA CAGGGACACA
 421 GCAGGTTATA TTATTCTTTA TTGTCTCCCG ATGCTTGCTC TTCAACTTGC GGTTGTGTTG
 481 TCCGAGTCAC GCCTAAATGG TGGTAGTGGC TCTTATGTAA AGCTGCCACA CGACTTCACA
 541 AGAACGTATT CCCGAGTTAT TATTGATCAC GACGAGGTGG CCTTATGCAC ATATCCTCTA
 601 CTGAGTACCA TCCTTCTTGG TGTGTTTGCA GCCGTCCTAA CAGCTTACTT GTTCTGGCTT
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 781 ACAGCAGCAG ACAAGATTAT ATTCGAAGCC CTTTCTTTCT TGGCCTTCCT CTCCCTCTTC
 841 TGCTTTTGCG TGGTATCCAT CTGCTTGCTT GTCTACTTCC CGGTTTCAGA TTCCATGGCC
 901 CTGAGAGGTC TAAGAGACAC AGATGATGAG GATACGGCTG TGACCGAAGA ACGCAGTGGT
 961 GCTCTGTTAC TTGCACCAAA CTCTTCACAA ACTGATGAGG GATTGAGCTT AAGAGGTCGG
1021 AGAGACTCGG GATCGTCTAC ACAGGAGAGG TATGTGGAAC TCAGCCTATT TCTGGAAGCT
1081 GAGAACTAA
```


FIGURE 4 (contin.)

A. thaliana - contig t8123 - coordinates: 53392-54480 (C) http://mips.gsf.de/cgi-bin/proj/th..._gendna.pl?t8123/C/53392-54480/500

***A. thaliana* - contig t8123 - coordinates: 53392-54480 (C)** mips

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  241 tatcaagtgt taaagagtca agatcacaaa aagttctatc gggtgaccrg ggctgctttc
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  361 gtttctrcgt ttttcatcaa tgagtagtaa ctaatctgga aatttgttgg gagagaaagg
  421 gcacattgca ctgctattgc tagagarcgt ttctgcatcc atgctgytag agagcatgcg
  481 tggatactgt gttttgggtg ATGCCCCTGA CAAAATTAGT TCCCGATGCA TTCGGCGTTG
  541 TGACGATATG TCTAGTCGCT CTGCTAGTTC TTTTGGGTCT CCTTTGCATC GCTTACTCGT
  601 TCTATTTCCA GTCTCACGTT CGTAAGCAAG GCTATATTCA ACTTGGTTAC TTCAGTGGTC
  661 CCTGGATTAT CCGAATCACT TTCATTCTCT TTGCTATCTG GTGGGCTGTT GGTGAGATTT
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  841 TTCTGACTCT CATGTTTCTT CTGCGTGCTC CCTTGAAGAT GGAATCAGGG GCTTTGAGCG
  901 GAAAATGGAA CAGGGACACA GCAGGTTATA TTATTCTTTA TTGTCTCCCG ATGCTTGCTC
  961 TTCAACTTGC GGTTGTGTTG TCCGAGTCAC GCCTAAATGG TGGTAGTGGC TCTTATGTAA
 1021 AGCTGCCACA CGACTTCACA AGAACGTATT CCCGAGTTAT TATTGATCAC GACGAGGTGG
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 1441 TGACCGAAGA ACGCAGTGGT GCTCTGTTAC TTGCACCAAA CTCTTCACAA ACTGATGAGG
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Sequences of 5' leader, 3' trailer, and introns (when applicable) are printed in lowercase.

FIGURE 4 (contin.)

047-E2F-PROV.ST25
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<120> Identification of novel E2F target genes and use thereof

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<160> 105

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<213> Arabidopsis thaliana

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<211> 1506

<212> DNA

<213> Arabidopsis thaliana

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cttaattga 1869

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<211> 1257

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<213> Arabidopsis thaliana

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<211> 219

<212> DNA

<213> Arabidopsis thaliana

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<210> 26

<211> 576

<212> DNA

<213> Arabidopsis thaliana

<400> 26
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<211> 639

<212> DNA

<213> Arabidopsis thaliana

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047-E2F-PROV.ST25

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<212> DNA

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<212> DNA

<213> Arabidopsis thaliana

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<211> 1680

<212> DNA

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<211> 981

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ccaaaacaag cgggatatga gaagaggagg gatctgtatt tgctctatca ttacttgaac 900

cattataacc tgtttggctc gggctaccga tcatctgcga tgtcaatcat cgatgattat 960

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<210> 33

<211> 237

<212> DNA

<213> Arabidopsis thaliana

<400> 33

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accgactgcg aggagcacaa aaagaagctc ccgaccaacc ttagccgtaa cggcggtgca 180

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<212> DNA

<213> Arabidopsis thaliana

<400> 34

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tcgtgcgcat tgatccgtga cgaaatcgac ctgattccgg ttcagagccg agatcggacc 180

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<210> 35

<211> 537

<212> DNA

<213> Arabidopsis thaliana

<400> 35

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gggcaacatg accagaagaa aactcatgag acaaacagtg gtcttaatgg ccttggaatg 420

ttcattaaca atggtgagaa gaaacatagg aggaaaagtg agcacaagaa gaagaacaag 480

gatgggcatg gcagtggtaa tgagagtgga agcagcagcg gtagcgacag cgactga 537

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<212> DNA

<213> Arabidopsis thaliana

<400> 36

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gtcgccggcg aaggtagtcg gaagaagcta gagaggaaga agagccaagt gttactggaa 180

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gtggaagatt gtccgtcgcc tccactggtc accgccactc cgattgccaa ttggaagatc 480

tctagtcccg gtgataatcc ggatgatgtg aaagctaggc tcaaatactg ggcacaagcc 540

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acttgctga 609

<210> 37

<211> 1917

<212> DNA

<213> Arabidopsis thaliana

<400> 37

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cgtctgtctg ctcttgaaac cgccatgcgt cctactcaga ttaggactca tgctataagg 180

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cgcctatttg atggccttcc caactcactg agaccatcct cagacgggga tggaggtgga 540

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cctttggttg agagtgggaa gaatcctcag aaatacataa agtatacagc tgaagatctt 1860

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<210> 38

<211> 1581

<212> DNA

<213> Arabidopsis thaliana

<400> 38

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aaaccgttcc tccctcttgt tctccagctt cttcaagaac taatcacccg ttcccctacc 300

acacacgacg gcgcgtgcac aaagtttgaa caacttgaaa tcaaaccaag tccagttagc 360

tgggtcatgg actctcactc acctgaatcc tcctcatcag tctttaatct aatcctcctc 420

acacgcctct tctggttgtg tgtgtttgac gcgccaagcg aagtaggctc tttcttcttc 480

caacacttac taggtccaca cgtgaacgcg cttacatgtc aacatgcacc tgtcttacgg 540

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aagttgaaca ctttgtttta tgagactaga tgtgtagagt ggtgtgatga ggttgatttg 1560

ccgttgcttc ctacttctta g 1581

<210> 39

<211> 921

<212> DNA

<213> Arabidopsis thaliana

<400> 39

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tatggttttt ggaaatgggg agctttgatt atcgcatttc tagcttattt caccaacttt 180

gttagtaaac tcaacagtct agttgttagg ttaagaaaaa tagatgtctc tgtttcctct 240

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aagtttaacg gtgtgttgac ggacttgacg gaatgtgagg ctgagacttg gtgggacgct 900

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<211> 999

<212> DNA

<213> Arabidopsis thaliana

<400> 40

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<211> 3267

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<213> Arabidopsis thaliana

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tatacactta attcactaat ttatactttt ttctaa 816

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gaagacactg agattgataa caacgaagct ccggatgacc aagcctgcgc atcagctgtg 360

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<213> Arabidopsis thaliana

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tttaagcctc caccaccgcg aatctgcggc catcctaacg gtcctccggt tacttctccg 120

agaatcaagc tcagtgatgg aagatatctt gcttatagag aatctggggt tgatagagac 180

aatgctaact acaagatcat tgtcgttcat ggcttcaaca gctccaaaga cactgaattt 240

cccatcccta aggatgtaat tgaggagctt gggatatact ttgtgttcta cgatagagca 300

ggatatggag aaagtgatcc acacccatca cgcactgtta agagtgaagc atacgacatt 360

caagaactcg ccgataaact caagatcgga ccaaagttct atgttcttgg tatatcacta 420

ggtgcttact cggtttatag ttgcctcaaa tacattcccc acagactagc tggagcagtc 480

ttaatggttc catttgtgaa ctattggtgg actaaagtgc ctcaagaaaa attgagtaaa 540

gcgttggagc taatgccaaa gaaagaccaa tggacgttta aagtggctca ttatgttccg 600

tggttgttat attggtggtt gacccaaaaa ctatttccgt cttcgagtat ggtcacgggg 660

aacaatgcgt tatgcagcga caaagatttg gtcgtcataa agaagaaaat ggagaatcca 720

cgccctggct tggaaaaagt tagacaacaa ggagaccatg aatgtcttca ccgggacatg 780

atagccggat tcgcgacatg ggaattcgac ccgactgaat tagaaaatcc gtttgcggaa 840

ggcgaaggat cggtccacgt ttggcaaggg atggaagaca gaatcattcc atacgaaatt 900

aatcgatata tatcagagaa gcttccatgg attaagtacc atgaggtctt aggttatgga 960

catcttctaa acgccgagga ggagaaatgc aaagacatta tcaaggcact tcttgtcaac 1020

tga 1023

<210> 46

<211> 981

<212> DNA

<213> Arabidopsis thaliana

<400> 46
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ggtcgtgatt tggaaattag acctggtggt atgttggttc agaaacgtaa cccggatttg 120

gatcctgtcg gacctccacc accaccgatg atcagagtta gaatcaagta cggtgccgtc 180

taccatgaga tcaatattag tcctcaagct tcttttgggg agctaaagaa gatgttgact 240

ggaccaacgg gtattcatca tcaagatcag aagctaatgt ataaagataa agagagggat 300

tcgaaggcgt tcctcgatgt ttcgggagtg aaagataaat ctaagatggt gcttatagaa 360

gacccgctta gccaagagaa acggtttttg gagatgagga agattgctaa aaccgaaaag 420

gcgtctaaag cgatatcgga tattagcctt gaagttgata ggctcggcgg acgagtttcg 480

gcttttgaga tggtaactaa aaaaggaggg aagattgcgg agaaagatct tgtaacggtt 540

atcgaattgc tgatgaatga gttgattaag ttcgatgcga ttgtagctga aggagatgtc 600

aagttacaaa gaaagatgca ggtgaagaga gtgcagaatt atgtggaaac actcgatgcc 660

ttgaaggtga aaaactccat ggctaatggg caacagaaac agtcaagtac tgctcagaga 720

cttgcaccga ttcaagaaca taacaatgaa gagagacaag aacagaaacc gatacaatcg 780

ctcatggaca tgccgataca atacaaagag aagaagcaag agattgaaga ggagcctagg 840

aattcagggg aaggaccatt tgtgttagat tcttctggta aatgggaaac attcgatcat 900

catcccgtga cgccattgag ctcgactact gcgaaaaata acgcgatccc gcccaggttt 960

aattgggaat tctttgattg a 981

<210> 47

<211> 570

<212> DNA

<213> Arabidopsis thaliana

<400> 47

atggcgaaat ctccggtgga agtgaatttg attcctatcg aagctactcc ggagaacttc 60

gcagagtatg gtcaagtcat tgaagcctct cgtgatggtg ctggtttcgg tccccacgac 120

gctcaactag atctctctag aggaacccca cggctcttata tacttaggct gaaagaaaca 180

cccttagggt ttttcaagat cacacatcac gcaaaggtga cacagtgtct aggatcaata 240

ggaggtgatg tttggtatat gggagtggct aagccgtctc ttattgaaga tgatgacgat 300

gatggaagga gcgtagatac agtaaaatca aagtctggtc acttatacat tccacctgag 360

gtggaagaga ttcgcgtctt caggttctcg ggacgaaagt ttgtgaaact gcaccgtggt 420

acatggcatg ctggaccctt gtttagtggc agctcgttca tggatttcta caacttagag 480

ctcagcaaca caaatgtggt ggatcacacg tcacgatgatt tcaccaagaa taatggagtc 540

agcttcggat ttgacacatt gtcttcctag 570

<210> 48

<211> 549

<212> DNA

<213> Arabidopsis thaliana

<400> 48
atggcgtcgt cgctgcaaag ctcggggatg ttgacgaaag agcaaatggt ttatctcttt 60

gatcgattcg attacttgac ttcacaatct gatgtgaaga aacgaatctc cgacgctgtg 120

gatgacaaac aggaagctgt agcggtaaca actgctattc aagaggagat attcttggag 180

atggggattg acccgggatt tggtattggc tgcttgggaa agctgaactc tgcatacgaa 240

aacgataaag agttgatgat tggtttctac aagtttctcg caaaggagga gatggcatgt 300

gaagaagctg agcttggaca agatggattt gaacagaaaa tgaaagcact acaacaatta 360

caagaacagc aactagagat gcttaagtat atgcgtaaat tctctctgga tgatcaatct 420

gctatccttc aaaagcttca gaagcaatta gaaaatgcgg gttttgagcc ggaggcgtct 480

cttttgtcag gagaggaaat ggaggaagct ggaagaagaa gagtttcacc tgtttttgga 540

agcagatag 549

<210> 49

<211> 327

<212> DNA

<213> Arabidopsis thaliana

<400> 49
atggctatca tcgcaagcac gttcggcacg gggctaagtt acgccgggga gcttccattc 60

aagccagtca ccgggggaga ggtgggacga aagcagcaga gaatggtggt ggtgagagca 120

gaaggcggtg gaggtatcaa tccggagatc agaaagaacg aagataaggt tgttgactcc 180

gtcgttgtca ccgagctttc caagaacata actccctatt gcaggtgttg gaggtcgggg 240

acgtttccat tgtgtgatgg gagtcatgtg aagcacaaca aagctaatgg agataacgtt 300

ggccctcttc ttctcaagaa acagtag 327

<210> 50

<211> 558

<212> DNA

<213> Arabidopsis thaliana

<400> 50
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ctcttcctca ctgcaaacta cgtcctcctc ggtgcatcgt caagctgcat cttcctcact 120
ctctctctcc gtctaatccc ttcactctgc ggtttcttcc tcatcctcct tcacgccacc 180
acgatcgcag ccgccgtctc aggctgtgca gccgcatctt atggtaagaa ccggtggtac 240
gcagctcaca tgatcgcaac tgtccttacc gccattttcc aaggctcagt ctctgttctc 300
atctttacca acacttcgaa tttcctcgag agccttaact cttacgtccg tgagaaagaa 360
gcgtctatga tcttgaaact agctggtggg ctctgtgttg taatcttttg ccttgagtgg 420
atcgttcttg ttctcgcctt tttcttgaag tactacgctt atgtcgatgg tgataacaat 480
ggagttgcta tgaaaaggac tggtaaggtt cagagtgaag agactctcaa aaattcccca 540
tgggcgttcc aagtttga 558

<210> 51
<211> 546
<212> DNA
<213> Arabidopsis thaliana

<400> 51
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gctttcgccg aagatgatcc agactgtgta tacacattct acctcagaac cggatcgatc 120
tggaaagccg gaaccgattc gatcatcagc gcaagaatct acgataagga cggtgactac 180
atcggaatca aaaaccttca agcttgggct ggattaatgg gacctgatta caattacttc 240
gagaggggta atctcgacat tttcagtgga agagcaccgt gtttacctag tccgatctgt 300
gccttaaacc taacctccga tggctccggc gatcaccatg gttggtacgt taattacgtt 360
gagatcacga cggctggtgt tcacgcacag tgctcgacgc aggattttga gattgagcaa 420
tggctcgcta ctgatacttc tccttatgag ctcaccgccg tacggaacaa ttgtccggtc 480
aagcttaggg atagtgttag tcgggtcggg tctgagattc ggaaaaagct ttcttgggtc 540
gtttaa 546

<210> 52
<211> 1110
<212> DNA

<213> Arabidopsis thaliana

<400> 52

atgttgggtg ctggatttca gttgacgaga ggcagacacg gcgacgatcc tttctacact 60

tccgcaaaaa ctcgcagggc caatcagcgc atcgatcagc tccgtagagc tcagagcgac 120

gtctctaacg ttccatcatc agctccttct ccgcataaac aacaactcga gccgtccgat 180

ttatcttcca gtaatctaga tcggttttta gagtcggtca caccatccgt accggctcag 240

tttttatcca agacattgct acgagaaaga agagcagatg atgattataa taaacttgtg 300

ccttattttg tgcttggtga tatatgggac tcatttgcag agtggagtgc ttacggcacc 360

ggtgtgcctc ttgttttgaa taacaacaag gatcgtgtta tccaatacta tgtcccttct 420

ttgtcagcca ttcaaatcta tgctcattct catgccttgg attcatctct taaatcaagg 480

cgtcctggtg atagtagcga cagtgatttt cgggattcaa gtagcgatgt tagcagcgat 540

agtgattccg agcgggtttc tgctagagta gactgtatct cattgaggga tcaacatcag 600

gaagactctt ccagtgatga tggcgaacct ttaggctctc aaggtcgttt gatgtttgag 660

tatcttgaaa gagaccttcc atacatccgt gaacctttg ctgataaggt cttggacctc 720

gcagctcagt ttcccgagct aatgacgctg agaagctgtg acttacttcg gtcaagctgg 780

ttttctgttg catggtaccc aatttacaga atacccacag gaccgacact gaaggacctg 840

gatgcttgtt tcttgacgta tcattcccta cacacatctt ttggaggtga aggcagtgaa 900

caatcaatga gccttacgca accaagggag agcgagaaga tgtcattgcc tgtgtttggg 960

cttgcttcat acaagttcag aggttcatta tggacaccca ttgggggttc ggagcaccag 1020

ctcgtgaact ctctgttcca agccgctgac aaatggctgc attcttgtca tgtcagccac 1080

cctgatttcc tcttcttctg ccgtcgttga 1110

<210> 53

<211> 362

<212> PRT

<213> Arabidopsis thaliana

<400> 53

Met Pro Leu Thr Lys Leu Val Pro Asp Ala Phe Gly Val Val Thr Ile
1 5 10 15

Cys Leu Val Ala Leu Leu Val Leu Leu Gly Leu Leu Cys Ile Ala Tyr
20 25 30

Ser Phe Tyr Phe Gln Ser His Val Arg Lys Gln Gly Tyr Ile Gln Leu
35 40 45

Gly Tyr Phe Ser Gly Pro Trp Ile Ile Arg Ile Thr Phe Ile Leu Phe
50 55 60

Ala Ile Trp Trp Ala Val Gly Glu Ile Phe Arg Leu Ser Leu Leu Arg
65 70 75 80

Arg His Arg Arg Leu Leu Ser Gly Leu Asp Leu Arg Trp Gln Glu Asn
85 90 95

Val Cys Lys Trp Tyr Ile Val Ser Asn Leu Gly Phe Ala Glu Pro Cys
100 105 110

Leu Phe Leu Thr Leu Met Phe Leu Leu Arg Ala Pro Leu Lys Met Glu
115 120 125

Ser Gly Ala Leu Ser Gly Lys Trp Asn Arg Asp Thr Ala Gly Tyr Ile
130 135 140

Ile Leu Tyr Cys Leu Pro Met Leu Ala Leu Gln Leu Ala Val Val Leu
145 150 155 160

Ser Glu Ser Arg Leu Asn Gly Gly Ser Gly Ser Tyr Val Lys Leu Pro
165 170 175

His Asp Phe Thr Arg Thr Tyr Ser Arg Val Ile Ile Asp His Asp Glu
180 185 190

Val Ala Leu Cys Thr Tyr Pro Leu Leu Ser Thr Ile Leu Leu Gly Val
195 200 205

Phe Ala Ala Val Leu Thr Ala Tyr Leu Phe Trp Leu Gly Arg Gln Ile
210 215 220

Leu Lys Leu Val Ile Asn Lys Arg Leu Gln Lys Arg Val Tyr Thr Leu
225 230 235 240

Ile Phe Ser Val Ser Ser Phe Leu Pro Leu Arg Ile Val Met Leu Cys
245 250 255

Leu Ser Val Leu Thr Ala Ala Asp Lys Ile Ile Phe Glu Ala Leu Ser
260 265 270

Phe Leu Ala Phe Leu Ser Leu Phe Cys Phe Cys Val Val Ser Ile Cys
275 280 285

Leu Leu Val Tyr Phe Pro Val Ser Asp Ser Met Ala Leu Arg Gly Leu
290 295 300

Arg Asp Thr Asp Asp Glu Asp Thr Ala Val Thr Glu Glu Arg Ser Gly
305 310 315 320

Ala Leu Leu Leu Ala Pro Asn Ser Ser Gln Thr Asp Glu Gly Leu Ser
325 330 335

Leu Arg Gly Arg Arg Asp Ser Gly Ser Ser Thr Gln Glu Arg Tyr Val
340 345 350

Glu Leu Ser Leu Phe Leu Glu Ala Glu Asn
355 360

<210> 54

<211> 72

<212> PRT

<213> Arabidopsis thaliana

<400> 54

Met Glu Leu Pro Ser Pro Tyr Ser Ser Arg Lys Glu Glu Ser Thr Val
1 5 10 15

Pro Pro Lys Arg Gly Arg Val Lys Ile Met Ile Phe Arg Asp Leu Val
20 25 30

Arg Ser Glu Thr Ser Met Ala Pro Thr Pro Arg Arg Gly Arg Ile Lys
35 40 45

Lys Met Ile Ala Gly Asp Leu Val Gly Ser Gly Lys Gln Asn Asn Tyr
50 55 60

Asp Gly Asp Gly Lys Arg Gly Gly
65 70

<210> 55

<211> 263

<212> PRT

<213> Arabidopsis thaliana

<400> 55

Met Arg Met Ser Cys Asn Gly Cys Arg Val Leu Arg Lys Gly Cys Ser
1 5 10 15

Glu Asp Cys Ser Ile Arg Pro Cys Leu Ala Trp Ile Lys Ser Pro Glu
20 25 30

Ala Gln Ala Asn Ala Thr Val Phe Leu Ala Lys Phe Tyr Gly Arg Ala
35 40 45

Gly Leu Met Asn Leu Ile Asn Ala Gly Pro Asn His Leu Arg Pro Gly
50 55 60

Ile Phe Arg Ser Leu Leu His Glu Ala Cys Gly Arg Ile Val Asn Pro
65 70 75 80

Ile Tyr Gly Ser Val Gly Leu Leu Trp Ser Gly Asn Trp Gln Leu Cys
85 90 95

Gln Asp Ala Val Glu Ala Val Met Lys Gly Glu Pro Val Lys Glu Ile
100 105 110

Ala Thr Asp Ala Ala Thr Ile Gly Gln Gly Pro Pro Leu Lys Ile Tyr
115 120 125

Asp Ile Arg His Ile Ser Lys Asp Asp Asn Ser Ala Ala Ala Ala Thr
130 135 140

Gly Ser Thr Asp Leu Lys Leu Ala Lys Thr Arg Arg Ala Lys Arg Val
145 150 155 160

Ser Thr Val Ala Ile Gln Ala Glu Ser Glu Gly Lys Ser Asp Glu Ala
165 170 175

Ser His Asp Ser Ser Leu Ser His Gln Ser Glu Ile Val Ala Ala His
180 185 190

Glu Gly Glu Ser Lys Glu Ser Glu Ser Asn Val Ser Glu Val Leu Ala
195 200 205

Phe Ser Pro Pro Ala Val Lys Gly Ser Gly Glu Ile Lys Leu Asp Leu
210 215 220

Thr Leu Arg Leu Glu Pro Val Ser Arg Ala Tyr His Val Val Pro Val
225 230 235 240

Lys Lys Arg Arg Ile Gly Val Phe Gly Thr Cys Gln Lys Glu Ser Thr
245 250 255

Cys Lys Thr Glu Leu Met Leu
260

<210> 56

<211> 156

<212> PRT

<213> Arabidopsis thaliana

<400> 56

Met Gly Ala Cys Ala Ser Arg Glu Ser Leu Arg Ser Asp Ser Ala Lys
1 5 10 15

Leu Ile Leu Leu Asp Gly Thr Leu Gln Glu Phe Ser Ser Pro Val Lys
20 25 30

Val Trp Gln Ile Leu Gln Lys Asn Pro Thr Ser Phe Val Cys Asn Ser
35 40 45

Asp Glu Met Asp Phe Asp Asp Ala Val Ser Ala Val Ala Gly Asn Glu
50 55 60

Glu Leu Arg Ser Gly Gln Leu Tyr Phe Val Leu Pro Leu Thr Trp Leu
65 70 75 80

Asn His Pro Leu Arg Ala Glu Glu Met Ala Ala Leu Ala Val Lys Ala
85 90 95

Ser Ser Ala Leu Thr Lys Ser Gly Gly Val Gly Trp Val Ser Gly Asp
100 105 110

Asp Asp Val Thr Thr Ser Glu Lys Thr Tyr Gln Lys Lys Asn Ile Ala
115 120 125

Gly Val Lys Thr Asn Gly Gly Gly Gly Arg Gly Cys Gly Lys Gly Lys
130 135 140

Arg Arg Phe Thr Ala Asn Leu Ser Thr Ile Ala Glu
145 150 155

<210> 57

<211> 207

<212> PRT

<213> Arabidopsis thaliana

<400> 57

Met Leu Ala Val His Arg Pro Ser Ser Ala Val Ser Asp Gly Asp Ser
1 5 10 15

Val Gln Ile Pro Met Met Ile Ala Ser Phe Gln Lys Arg Phe Pro Ser
20 25 30

Leu Ser Arg Asp Ser Thr Ala Ala Arg Phe His Thr His Glu Val Gly
35 40 45

Pro Asn Gln Cys Cys Ser Ala Val Ile Gln Glu Ile Ser Ala Pro Ile
50 55 60

Ser Thr Val Trp Ser Val Val Arg Arg Phe Asp Asn Pro Gln Ala Tyr
65 70 75 80

Lys His Phe Leu Lys Ser Cys Ser Val Ile Gly Gly Asp Gly Asp Asn
85 90 95

Val Gly Ser Leu Arg Gln Val His Val Val Ser Gly Leu Pro Ala Ala
100 105 110

Ser Ser Thr Glu Arg Leu Asp Ile Leu Asp Asp Glu Arg His Val Ile
115 120 125

Ser Phe Ser Val Val Gly Gly Asp His Arg Leu Ser Asn Tyr Arg Ser
130 135 140

Val Thr Thr Leu His Pro Ser Pro Ile Ser Gly Thr Val Val Val Glu
145 150 155 160

Ser Tyr Val Val Asp Val Pro Pro Gly Asn Thr Lys Glu Glu Thr Cys
165 170 175

Asp Phe Val Asp Val Ile Val Arg Cys Asn Leu Gln Ser Leu Ala Lys
180 185 190

Ile Ala Glu Asn Thr Ala Ala Glu Ser Lys Lys Lys Met Ser Leu
195 200 205

<210> 58

<211> 190

<212> PRT

<213> Arabidopsis thaliana

<400> 58

Met Ser Glu Gly Ser Glu Asp Thr Lys Thr Lys Leu Asp Ser Ala Gly
1 5 10 15

Glu Leu Ser Asp Val Asp Asn Glu Asn Cys Ser Ser Ser Gly Ser Gly
20 25 30

Gly Gly Ser Ser Ser Gly Asp Thr Lys Arg Thr Cys Val Asp Cys Gly
35 40 45

Thr Ile Arg Thr Pro Leu Trp Arg Gly Gly Pro Ala Gly Pro Lys Ser
50 55 60

Leu Cys Asn Ala Cys Gly Ile Lys Ser Arg Lys Lys Arg Gln Ala Ala
65 70 75 80

Leu Gly Met Arg Ser Glu Glu Lys Lys Lys Asn Arg Lys Ser Asn Cys
85 90 95

Asn Asn Asp Leu Asn Leu Asp His Arg Asn Ala Lys Lys Tyr Lys Ile
100 105 110

Asn Ile Val Asp Asp Gly Lys Ile Asp Ile Asp Asp Asp Pro Lys Ile
115 120 125

Cys Asn Asn Lys Arg Ser Ser Ser Ser Ser Ser Asn Lys Gly Val Ser
130 135 140

Lys Phe Leu Asp Leu Gly Phe Lys Val Pro Val Met Lys Arg Ser Ala
145 150 155 160

Val Glu Lys Lys Arg Leu Trp Arg Lys Leu Gly Glu Glu Glu Arg Ala
165 170 175

Ala Val Leu Leu Met Ala Leu Ser Cys Ser Ser Val Tyr Ala
180 185 190

<210> 59

<211> 526

<212> PRT

<213> Arabidopsis thaliana

<400> 59

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Met Ala Val Tyr Pro Asn Val Asn Gly Asp Lys Lys His Trp Trp Phe
1               5                  10                  15

Thr His Arg Lys Leu Val Asp Lys Tyr Ile Lys Asp Ala Thr Thr Leu
            20                  25                  30

Met Ala Ser Glu Glu Ala Asn Asp Val Ala Ser Ala Leu His Leu Leu
        35                  40                  45

Asp Ala Ala Leu Ser Ile Ser Pro Arg Leu Glu Thr Ala Leu Glu Leu
    50                  55                  60

Lys Ala Arg Ser Leu Leu Phe Leu Arg Arg Phe Lys Asp Val Ala Asp
65                  70                  75                  80

Met Leu Gln Asp Tyr Ile Pro Ser Leu Lys Leu Asp Asp Glu Gly Ser
                85                  90                  95

Ala Ser Ser Gln Gly Ser Ser Ser Ser Asp Gly Ile Asn Leu Leu Ser
            100                 105                 110

Asp Ala Ser Ser Pro Gly Ser Phe Lys Cys Phe Ser Val Ser Asp Leu
        115                 120                 125

Lys Lys Lys Val Met Ala Gly Ile Cys Lys Lys Cys Asp Lys Glu Gly
    130                 135                 140

Gln Trp Arg Tyr Val Val Leu Gly Gln Ala Cys Cys His Leu Gly Leu
145                 150                 155                 160

Met Glu Asp Ala Met Val Leu Leu Gln Thr Gly Lys Arg Leu Ala Ser
                165                 170                 175

Ala Glu Phe Arg Arg Arg Ser Ile Cys Trp Ser Asp Asp Ser Phe Leu
            180                 185                 190

Leu Leu Ser Glu Ser Ser Ser Ala Ser Ser Pro Pro Pro Glu Ser Glu
        195                 200                 205

Asn Phe Thr His Leu Leu Ala His Ile Lys Leu Leu Leu Arg Arg Arg
    210                 215                 220

Ala Ala Ala Ile Ala Ala Leu Asp Ala Gly Leu Phe Ser Glu Ser Ile
225                 230                 235                 240

Arg His Phe Ser Lys Ile Val Asp Gly Arg Arg Pro Ala Pro Gln Gly
                245                 250                 255
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Phe Leu Ala Glu Cys Tyr Met His Arg Ala Ala Ala Tyr Arg Ser Ala
260 265 270

Gly Arg Ile Ala Glu Ala Ile Ala Asp Cys Asn Lys Thr Leu Ala Leu
275 280 285

Glu Pro Ser Cys Ile Gln Ala Leu Glu Thr Arg Ala Ala Leu Leu Glu
290 295 300

Thr Val Arg Cys Phe Pro Asp Ser Leu His Asp Leu Glu His Leu Lys
305 310 315 320

Leu Leu Tyr Asn Thr Ile Leu Arg Asp Arg Lys Leu Pro Gly Pro Val
325 330 335

Trp Lys Arg His Asn Val Lys Tyr Arg Glu Ile Pro Gly Lys Leu Cys
340 345 350

Val Leu Thr Thr Lys Thr Gln Lys Leu Lys Gln Lys Ile Ala Asn Gly
355 360 365

Glu Thr Gly Asn Val Asp Tyr Tyr Gly Leu Ile Gly Val Arg Arg Gly
370 375 380

Cys Thr Arg Ser Glu Leu Asp Arg Ala His Leu Leu Leu Cys Leu Arg
385 390 395 400

Tyr Lys Pro Asp Arg Ala Ser Ser Phe Ile Glu Arg Cys Glu Phe Thr
405 410 415

Asp Gln Asn Asp Val Asp Ser Val Arg Asp Arg Ala Lys Met Ser Ser
420 425 430

Leu Leu Leu Tyr Arg Leu Ile Gln Lys Gly Tyr Thr Ala Val Thr Ala
435 440 445

Ile Ile Ala Glu Glu Gln Arg Lys Asn Ala Ile Ala His Ala Gln Lys
450 455 460

Ile Glu Glu Arg Lys Pro Val Glu Lys Ser Gly Ser Ile Lys Arg Thr
465 470 475 480

Gly Asn Ala Glu Thr Lys Pro Val Asn Ser Asn Ala Tyr Gln Gly Val
485 490 495

Phe Cys Arg Asp Leu Ala Ala Val Gly Asn Leu Leu Thr Arg Ala Gly
500 505 510

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Phe Asn His Pro Ile Pro Val Lys Tyr Glu Ala Leu Thr Cys
515 520 525

<210> 60

<211> 387

<212> PRT

<213> Arabidopsis thaliana

<400> 60

Met Ile Ser Leu Arg Leu Phe Glu Ser Phe Ser Gln Ala Lys Glu Ala
1 5 10 15

Val Lys Val Leu Lys Lys Arg Leu Gly Ser Lys Asn Ser Lys Val Gln
20 25 30

Ile Leu Ala Leu Tyr Pro Glu Leu Asn Val Arg Glu Lys Ile Leu Thr
35 40 45

Leu Leu Asp Thr Trp Gln Glu Ala Phe Gly Gly Arg Gly Gly Arg Tyr
50 55 60

Pro Gln Tyr Tyr Asn Ala Tyr Asn Asp Leu Arg Ser Ala Gly Ile Glu
65 70 75 80

Phe Pro Pro Arg Thr Glu Ser Ser Leu Ser Phe Phe Thr Pro Pro Gln
85 90 95

Thr Gln Pro Asp Glu Asp Ala Ala Ile Gln Ala Ser Leu Gln Gly Asp
100 105 110

Asp Ala Ser Ser Leu Ser Leu Glu Glu Ile Gln Ser Ala Glu Gly Ser
115 120 125

Val Asp Val Leu Met Asp Met Leu Gly Ala His Asp Pro Gly Asn Pro
130 135 140

Glu Ser Leu Lys Glu Glu Val Ile Val Asp Leu Val Glu Gln Cys Arg
145 150 155 160

Thr Tyr Gln Arg Arg Val Met Thr Leu Val Asn Thr Thr Thr Asp Glu
165 170 175

Glu Leu Leu Cys Gln Gly Leu Ala Leu Asn Asp Asn Leu Gln His Val
180 185 190

Leu Gln Arg His Asp Asp Ile Ala Asn Val Gly Ser Val Pro Ser Asn
195 200 205

Gly Arg Asn Thr Arg Ala Pro Pro Pro Val Gln Ile Val Asp Ile Asn
210 215 220

His Asp Asp Glu Asp Asp Glu Ser Asp Asp Glu Phe Ala Arg Leu Ala
225 230 235 240

His Arg Ser Ser Thr Pro Thr Arg Arg Pro Val His Gly Ser Asp Ser
245 250 255

Gly Met Val Asp Ile Leu Ser Gly Asp Val Tyr Lys Pro Gln Gly Asn
260 265 270

Ser Ser Ser Gln Gly Val Lys Lys Pro Pro Pro Pro Pro Pro His Thr
275 280 285

Ser Ser Ser Ser Ser Ser Pro Val Phe Asp Asp Ala Ser Pro Gln Gln
290 295 300

Ser Lys Ser Ser Glu Val Ile Arg Asn Leu Pro Pro Pro Pro Ser Arg
305 310 315 320

His Asn Gln Arg Gln Gln Phe Phe Glu His His His Ser Ser Ser Gly
325 330 335

Ser Asp Ser Ser Tyr Glu Gly Gln Thr Arg Asn Leu Ser Leu Thr Ser
340 345 350

Ser Glu Pro Gln Lys Glu Glu Lys Pro Glu Asp Leu Leu Phe Lys Asp
355 360 365

Leu Val Glu Phe Ala Lys Thr Arg Ser Ser Lys Ala Asn Asn Asn Asn
370 375 380

Arg Ser Leu
385

<210> 61

<211> 650

<212> PRT

<213> Arabidopsis thaliana

<400> 61

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Met Glu Gly Gly Ser Val Asn Glu Ser His Ser Asn Ala Asp Gln Met
1               5                  10                  15

Phe Asp Thr Thr Ile Glu Glu Leu Cys Lys Asn Leu Cys Glu Leu Gln
            20                  25                  30

Ser Ser Asn Gln Ser Pro Ser Arg Gln Ser Phe Gly Ser Tyr Gly Asp
        35                  40                  45

Glu Ser Lys Ile Asp Ser Asp Leu Gln His Leu Ala Leu Gly Glu Met
    50                  55                  60

Arg Asp Ile Asp Ile Leu Glu Asp Glu Gly Asp Glu Asp Glu Val Ala
65                  70                  75                  80

Lys Pro Glu Glu Phe Asp Val Lys Ser Asn Ser Ser Asn Leu Asp Leu
                85                  90                  95

Glu Val Met Pro Arg Asp Met Glu Lys Gln Thr Gly Lys Lys Asn Val
            100                 105                 110

Thr Lys Ser Asn Val Gly Val Gly Gly Met Arg Lys Lys Lys Val Gly
        115                 120                 125

Gly Thr Lys Leu Gln Asn Gly Asn Glu Glu Pro Ser Ser Glu Asn Val
    130                 135                 140

Glu Leu Ala Arg Phe Leu Leu Asn Gln Ala Arg Asn Leu Val Ser Ser
145                 150                 155                 160

Gly Asp Ser Thr His Lys Ala Leu Glu Leu Thr His Arg Ala Ala Lys
                165                 170                 175

Leu Phe Glu Ala Ser Ala Glu Asn Gly Lys Pro Cys Leu Glu Trp Ile
            180                 185                 190

Met Cys Leu His Val Thr Ala Ala Val His Cys Lys Leu Lys Glu Tyr
        195                 200                 205

Asn Glu Ala Ile Pro Val Leu Gln Arg Ser Val Glu Ile Pro Val Val
    210                 215                 220

Glu Glu Gly Glu Glu His Ala Leu Ala Lys Phe Ala Gly Leu Met Gln
225                 230                 235                 240

Leu Gly Asp Thr Tyr Ala Met Val Gly Gln Leu Glu Ser Ser Ile Ser
                245                 250                 255
```

Cys Tyr Thr Glu Gly Leu Asn Ile Gln Lys Lys Val Leu Gly Glu Asn
260 265 270

Asp Pro Arg Val Gly Glu Thr Cys Arg Tyr Leu Ala Glu Ala Leu Val
275 280 285

Gln Ala Leu Arg Phe Asp Glu Ala Gln Gln Val Cys Glu Thr Ala Leu
290 295 300

Ser Ile His Arg Glu Ser Gly Leu Pro Gly Ser Ile Ala Glu Ala Ala
305 310 315 320

Asp Arg Arg Leu Met Gly Leu Ile Cys Glu Thr Lys Gly Asp His Glu
325 330 335

Asn Ala Leu Glu His Leu Val Leu Ala Ser Met Ala Met Ala Ala Asn
340 345 350

Gly Gln Glu Ser Glu Val Ala Phe Val Asp Thr Ser Ile Gly Asp Ser
355 360 365

Tyr Leu Ser Leu Ser Arg Phe Asp Glu Ala Ile Cys Ala Tyr Gln Lys
370 375 380

Ser Leu Thr Ala Leu Lys Thr Ala Lys Gly Glu Asn His Pro Ala Val
385 390 395 400

Gly Ser Val Tyr Ile Arg Leu Ala Asp Leu Tyr Asn Arg Thr Gly Lys
405 410 415

Val Arg Glu Ala Lys Ser Tyr Cys Glu Asn Ala Leu Arg Ile Tyr Glu
420 425 430

Ser His Asn Leu Glu Ile Ser Pro Glu Glu Ile Ala Ser Gly Leu Thr
435 440 445

Asp Ile Ser Val Ile Cys Glu Ser Met Asn Glu Val Glu Gln Ala Ile
450 455 460

Thr Leu Leu Gln Lys Ala Leu Lys Ile Tyr Ala Asp Ser Pro Gly Gln
465 470 475 480

Lys Ile Met Ile Ala Gly Ile Glu Ala Gln Met Gly Val Leu Tyr Tyr
485 490 495

Met Met Gly Lys Tyr Met Glu Ser Tyr Asn Thr Phe Lys Ser Ala Ile
500 505 510

Ser Lys Leu Arg Ala Thr Gly Lys Lys Gln Ser Thr Phe Phe Gly Ile
515 520 525

Ala Leu Asn Gln Met Gly Leu Ala Cys Ile Gln Leu Asp Ala Ile Glu
530 535 540

Glu Ala Val Glu Leu Phe Glu Glu Ala Lys Cys Ile Leu Glu Gln Glu
545 550 555 560

Cys Gly Pro Tyr His Pro Glu Thr Leu Gly Leu Tyr Ser Asn Leu Ala
565 570 575

Gly Ala Tyr Asp Ala Ile Gly Arg Leu Asp Asp Ala Ile Lys Leu Leu
580 585 590

Gly His Val Val Gly Val Arg Glu Glu Lys Leu Gly Thr Ala Asn Pro
595 600 605

Val Thr Glu Asp Glu Lys Arg Arg Leu Ala Gln Leu Leu Lys Glu Ala
610 615 620

Gly Asn Val Thr Gly Arg Lys Ala Lys Ser Leu Lys Thr Leu Ile Asp
625 630 635 640

Ser Asp Leu Thr Ser Ser Ser Ala Leu Arg
645 650

<210> 62

<211> 374

<212> PRT

<213> Arabidopsis thaliana

<400> 62

Met Gly Leu Glu Val Gly Ser Leu Cys Phe Lys Leu Lys Asp Gly Gly
1 5 10 15

Leu Thr Ser Arg Thr Asn Ser Phe Lys Arg Asp Asp Thr Asn Arg His
20 25 30

Gln Asn Ser Pro Lys Ser Thr Met Glu Arg Ser Leu Ser Phe Asn Ser
35 40 45

Trp Glu Val Pro Lys Glu Thr Lys Thr Asp Ser Asp Phe Glu Val Leu
50 55 60

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Glu Thr Lys Lys Ser Thr Pro Asn Thr Leu Asn Gly Arg Asn Cys Glu
65 70 75 80

Arg Ile Gln Ile Lys Lys Pro Thr Val Thr Pro Pro Glu Pro Phe Val
85 90 95

Phe Phe Ser Pro Arg Pro Val Thr Glu Leu Asp Ala Ala Ala Thr Thr
100 105 110

Leu Gln Lys Val Tyr Lys Ser Tyr Arg Thr Arg Arg Asn Leu Ala Asp
115 120 125

Cys Ala Val Val Val Glu Glu Leu Trp Trp Arg Thr Leu Glu Gly Ala
130 135 140

Ala Leu Asp Leu Ser Ser Val Ser Phe Phe Gly Glu Glu Lys His Glu
145 150 155 160

Thr Ala Val Ser Lys Trp Ala Arg Ala Arg Lys Arg Ala Ala Lys Val
165 170 175

Gly Lys Gly Leu Ser Lys Asp Glu Lys Ala Gln Lys Leu Ala Leu Gln
180 185 190

His Trp Leu Glu Ala Val Ser Pro His Asn Leu Asn Ile Phe Val Thr
195 200 205

Ser Tyr Gln Arg Gln Val Pro Tyr Leu Thr Ser Lys Ala Ile Ile Glu
210 215 220

Tyr Thr Leu Met Ile His Leu Leu Lys Leu Gln Ile Asp Pro Arg His
225 230 235 240

Arg Tyr Gly His Asn Leu His Phe Tyr Tyr Asp Val Trp Ser Ala Ser
245 250 255

Lys Ser Thr Gln Pro Phe Phe Tyr Trp Leu Asp Ile Gly Asp Gly Lys
260 265 270

Asp Val Asn Leu Glu Lys His Pro Arg Ser Val Leu Gln Lys Gln Cys
275 280 285

Ile Arg Tyr Leu Gly Pro Met Glu Arg Glu Ala Tyr Glu Val Ile Val
290 295 300

Glu Asp Gly Arg Leu Met Tyr Lys Gln Gly Met Thr Leu Ile Asn Ser
305 310 315 320

Thr Glu Glu Ala Lys Ser Ile Phe Val Leu Ser Thr Thr Arg Asn Leu
325 330 335

Tyr Val Gly Ile Lys Lys Lys Gly Leu Phe Gln His Ser Ser Phe Leu
340 345 350

Ser Gly Gly Ala Thr Thr Ala Ala Gly Arg Leu Val Ala Arg Asp Gly
355 360 365

Ile Leu Glu Val Leu Glu
370

<210> 63

<211> 324

<212> PRT

<213> Arabidopsis thaliana

<400> 63

Met Glu Cys Arg Ser Leu Asp Leu Thr Ile Ile Ser Ala Glu Asp Leu
1 5 10 15

Lys Asp Val Gln Leu Ile Gly Lys Gln Asp Leu Tyr Ala Val Val Ser
20 25 30

Ile Asn Gly Asp Ala Arg Thr Lys Gln Lys Thr Lys Val Asp Lys Asp
35 40 45

Cys Gly Thr Lys Pro Lys Trp Lys His Gln Met Lys Leu Thr Val Asp
50 55 60

Asp Ala Ala Ala Arg Asp Asn Arg Leu Thr Leu Val Phe Glu Ile Val
65 70 75 80

Ala Asp Arg Pro Ile Ala Gly Asp Lys Pro Val Gly Glu Val Ser Val
85 90 95

Pro Val Lys Glu Leu Leu Asp Gln Asn Lys Gly Asp Glu Glu Lys Thr
100 105 110

Val Thr Tyr Ala Val Arg Leu Pro Asn Gly Lys Ala Lys Gly Ser Leu
115 120 125

Lys Phe Ser Phe Lys Phe Gly Glu Lys Tyr Thr Tyr Gly Ser Ser Ser
130 135 140

Gly Pro His Ala Pro Val Pro Ser Ala Met Asp His Lys Thr Met Asp
145 150 155 160

Gln Pro Val Thr Ala Tyr Pro Pro Gly His Gly Ala Pro Ser Ala Tyr
165 170 175

Pro Ala Pro Pro Ala Gly Pro Ser Ser Gly Tyr Pro Pro Gln Gly His
180 185 190

Asp Asp Lys His Asp Gly Val Tyr Gly Tyr Pro Gln Gln Ala Gly Tyr
195 200 205

Pro Ala Gly Thr Gly Gly Tyr Pro Pro Pro Gly Ala Tyr Pro Gln Gln
210 215 220

Gly Gly Tyr Pro Gly Tyr Pro Pro Gln Gln Gln Gly Gly Tyr Pro Gly
225 230 235 240

Tyr Pro Pro Gln Gly Pro Tyr Gly Tyr Pro Gln Gln Gly Tyr Pro Pro
245 250 255

Gln Gly Pro Tyr Gly Tyr Pro Gln Gln Gln Ala His Gly Lys Pro Gln
260 265 270

Lys Pro Lys Lys His Gly Lys Ala Gly Ala Gly Met Gly Leu Gly Leu
275 280 285

Gly Leu Gly Ala Gly Leu Leu Gly Gly Leu Leu Val Gly Glu Ala Val
290 295 300

Ser Asp Ile Ala Asp Met Gly Asp Met Gly Asp Met Gly Asp Met Gly
305 310 315 320

Gly Phe Asp Phe

<210> 64

<211> 539

<212> PRT

<213> Arabidopsis thaliana

<400> 64

Met Ser Lys Asp Lys Val Ser Ser Pro Thr Ala Asp Leu Ile Pro Gln
1 5 10 15

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Leu Ala Ala Thr Leu Val Ala Ala Leu Gly Ala Gln Cys Tyr Arg Leu
20 25 30

Thr Leu Pro Pro Ser Pro Pro Pro Arg Ile Leu Thr Pro Gln Val Pro
35 40 45

Pro Ser Ser Ala Thr Met Ala Ser Ser Phe Asn Pro Thr Arg Ile Leu
50 55 60

Asp His Arg Ala Ser Ser His Arg Asn Arg Arg Gly Ala Phe Pro Ala
65 70 75 80

Ser Lys Arg Arg Arg Leu Val Asp Glu Pro Ile Asp Tyr Pro Asp Leu
85 90 95

Ser Asn Pro Ala Tyr Gln Val Leu Ser Thr Pro Leu Phe Ala Ser Gly
100 105 110

Ile Gly Ser Ile Arg Glu Leu Leu Ser Ser Ser Pro Pro Pro Thr Thr
115 120 125

Ser Ser Gln Pro Pro Ser Val Ser Ile Pro Pro Pro Ser Ala Pro Pro
130 135 140

Leu Val Leu Ser Asp Ser Lys Asp Ala Glu Pro Ala Gly Leu Thr Asn
145 150 155 160

Pro Ser Ala Pro Pro Ser Pro Leu Ala Pro Lys Asn Ile Thr Pro Val
165 170 175

Ala Ser Pro Val Ala Asp Val Pro Met Pro Asp Pro Leu Ile Ser Pro
180 185 190

Thr Ala Glu Thr Ala Glu Gly Ala Ser Val Pro Asp Ala Ala Val Ser
195 200 205

Tyr Ala Ala Arg Ala Ala Ala His Arg Gln Val Phe Ala Glu Arg Asp
210 215 220

Glu Leu Asp Arg Thr Leu Arg Arg Pro Leu Val Pro Pro His Thr Lys
225 230 235 240

Arg Phe Leu Ser Ala Ala Ala Ala Glu Arg Tyr Lys His Ile Ala Lys
245 250 255

Arg Asp Phe Ile Phe Gln Lys Thr Leu Pro Leu Asp Pro Glu Val Leu
260 265 270

Thr Ala Thr Lys Tyr Phe Leu Glu His Ser Gly Met Ala Gln Thr Val
275 280 285

Val Ala Val Glu Gln Phe Val Pro Glu Val Val Arg Glu Phe Tyr Ala
290 295 300

Asn Leu Pro Glu Met Glu Tyr Arg Glu Cys Gly Leu Asp Leu Val Tyr
305 310 315 320

Val Arg Gly Lys Met Tyr Glu Phe Ser Pro Ala Leu Ile Asn His Met
325 330 335

Phe Ser Ile Asp Asp Ser Ala Leu Asp Pro Glu Ala Pro Val Thr Leu
340 345 350

Ser Thr Ala Ser Arg Asp Asp Leu Ala Leu Met Met Thr Gly Gly Thr
355 360 365

Thr Arg Arg Trp Leu Arg Leu Gln Pro Ala Asp His Leu Asp Thr Met
370 375 380

Lys Met Leu His Lys Val Cys Cys Gly Asn Trp Phe Pro Thr Thr Asn
385 390 395 400

Thr Ser Thr Leu Arg Val Asp Arg Leu Arg Leu Ile Asp Met Gly Thr
405 410 415

His Gly Lys Ser Phe Asn Leu Gly Lys Leu Val Val Thr His Thr Met
420 425 430

Ser Leu Ala Arg Leu Gly Pro Leu Ser Ser His Arg Leu Ala Tyr Pro
435 440 445

Asn Leu Ile Tyr Gln Leu Leu Thr Phe Gln Arg Asp Val Arg Ser Arg
450 455 460

Pro Arg Asp Thr Leu Ser Asp Glu Pro Gly Val Phe Val Asn Asp Pro
465 470 475 480

Pro Pro Thr Gln Pro Thr Gln Ala Pro Pro Pro Met Gly His Lys Leu
485 490 495

Leu Leu Glu Asp Ile Asn Asp Leu Leu Glu Ile Gly Lys Arg Ile Arg
500 505 510

Arg Arg Leu Thr Gly Lys Leu Phe Ser Cys Phe Met Trp Cys Phe Ala
515 520 525

Tyr Cys Val Leu Ala Leu Cys Phe Leu Glu Phe
530 535

<210> 65

<211> 632

<212> PRT

<213> Arabidopsis thaliana

<400> 65

Met Ala Asp Glu Ser Gln Tyr Ser Ser Asp Thr Tyr Ser Asn Lys Arg
1 5 10 15

Lys Tyr Glu Glu Pro Thr Ala Pro Pro Pro Ser Thr Arg Arg Pro Thr
20 25 30

Gly Phe Ser Ser Gly Pro Ile Pro Ser Ala Ser Val Asp Pro Thr Ala
35 40 45

Pro Thr Gly Leu Pro Pro Ser Ser Tyr Asn Ser Val Pro Pro Pro Met
50 55 60

Asp Glu Ile Gln Ile Ala Lys Gln Lys Ala Gln Glu Ile Ala Ala Arg
65 70 75 80

Leu Leu Asn Ser Ala Asp Ala Lys Arg Pro Arg Val Asp Asn Gly Ala
85 90 95

Ser Tyr Asp Tyr Gly Asp Asn Lys Gly Phe Ser Ser Tyr Pro Ser Glu
100 105 110

Gly Lys Gln Met Ser Gly Thr Val Pro Ser Ser Ile Pro Val Ser Tyr
115 120 125

Gly Ser Phe Gln Gly Thr Thr Lys Lys Ile Asp Ile Pro Asn Met Arg
130 135 140

Val Gly Val Ile Ile Gly Lys Gly Gly Glu Thr Ile Lys Tyr Leu Gln
145 150 155 160

Leu Gln Ser Gly Ala Lys Ile Gln Val Thr Arg Asp Met Asp Ala Asp
165 170 175

Pro Asn Cys Ala Thr Arg Thr Val Asp Leu Thr Gly Thr Pro Asp Gln
180 185 190

Ile Ser Lys Ala Glu Gln Leu Ile Thr Asn Val Leu Gln Glu Ala Glu
195 200 205

Ala Gly Asn Thr Ala Gly Ser Gly Gly Gly Gly Gly Arg Arg Met Gly
210 215 220

Gly Gln Ala Gly Ala Asp Gln Phe Val Met Lys Ile Pro Asn Asn Lys
225 230 235 240

Val Gly Leu Ile Ile Gly Lys Gly Gly Glu Thr Ile Lys Ser Met Gln
245 250 255

Ala Lys Thr Gly Ala Arg Ile Gln Val Ile Pro Leu His Leu Pro Pro
260 265 270

Gly Asp Pro Thr Pro Glu Arg Thr Leu Gln Ile Asp Gly Ile Thr Glu
275 280 285

Gln Ile Glu His Ala Lys Gln Leu Val Asn Glu Ile Ile Ser Gly Glu
290 295 300

Asn Arg Met Arg Asn Ser Ala Met Gly Gly Gly Tyr Pro Gln Gln Gly
305 310 315 320

Gly Tyr Gln Ala Arg Pro Pro Ser Ser Trp Ala Pro Pro Gly Gly Pro
325 330 335

Pro Ala Gln Pro Gly Tyr Gly Gly Tyr Met Gln Pro Gly Ala Tyr Pro
340 345 350

Gly Pro Pro Gln Tyr Gly Gln Ser Pro Tyr Gly Ser Tyr Pro Gln Gln
355 360 365

Thr Ser Ala Gly Tyr Tyr Asp Gln Ser Ser Val Pro Pro Ser Gln Gln
370 375 380

Ser Ala Gln Gly Glu Tyr Asp Tyr Tyr Gly Gln Gln Gln Ser Gln Gln
385 390 395 400

Pro Ser Ser Gly Gly Ser Ser Ala Pro Pro Thr Asp Thr Thr Gly Tyr
405 410 415

Asn Tyr Tyr Gln His Ala Ser Gly Tyr Gly Gln Ala Gly Gln Gly Tyr
420 425 430

Gln Gln Asp Gly Tyr Gly Ala Tyr Asn Ala Ser Gln Gln Ser Gly Tyr
435 440 445

Gly Gln Ala Ala Gly Tyr Asp Gln Gln Gly Gly Tyr Gly Ser Thr Thr
450 455 460

Asn Pro Ser Gln Glu Glu Asp Ala Ser Gln Ala Ala Pro Pro Ser Ser
465 470 475 480

Ala Gln Ser Gly Gln Ala Gly Tyr Gly Thr Thr Gly Gln Gln Pro Pro
485 490 495

Ala Gln Gly Ser Thr Gly Gln Ala Gly Tyr Gly Ala Pro Pro Thr Ser
500 505 510

Gln Ala Gly Tyr Ser Ser Gln Pro Ala Ala Ala Tyr Asn Ser Gly Tyr
515 520 525

Gly Ala Pro Pro Pro Ala Ser Lys Pro Pro Thr Tyr Gly Gln Ser Gln
530 535 540

Gln Ser Pro Gly Ala Pro Gly Ser Tyr Gly Ser Gln Ser Gly Tyr Ala
545 550 555 560

Gln Pro Ala Ala Ser Gly Tyr Gly Gln Pro Pro Ala Tyr Gly Tyr Gly
565 570 575

Gln Ala Pro Gln Gly Tyr Gly Ser Tyr Gly Gly Tyr Thr Gln Pro Ala
580 585 590

Ala Gly Gly Gly Tyr Ser Ser Asp Gly Ser Ala Gly Ala Thr Ala Gly
595 600 605

Gly Gly Gly Gly Thr Pro Ala Ser Gln Ser Ala Ala Pro Pro Ala Gly
610 615 620

Pro Pro Lys Ala Ser Pro Lys Ser
625 630

<210> 66

<211> 704

<212> PRT

<213> Arabidopsis thaliana

<400> 66

Met Ala Trp Ser Ser Glu Thr Pro Ser Tyr Cys Gly Trp Asn Glu Arg
1 5 10 15

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His Val Lys Asn Thr Lys Glu Lys Met Glu Val His Tyr Tyr Leu Glu
20 25 30

Arg Lys Asp Gly Ile Ala Asp Leu Ala Val Ile Gly Arg Leu Lys Asn
35 40 45

Ser Lys Arg Met Ser Phe Arg Tyr Ala Leu Lys Lys Asn Arg Ser Val
50 55 60

Leu Lys Lys Leu Asn Ser Lys Asp Asp Val Ala Leu Trp Leu Asp Ser
65 70 75 80

Ile Val Ser Gly Glu Ile Pro His Val Ala Asp Val Pro Ala Thr Val
85 90 95

Met Thr Glu Lys Asp Ala Gly Gly Phe Asn Met Ser Thr Phe Met Asn
100 105 110

Arg Lys Phe Gln Glu Pro Ile Gln Gln Ile Lys Thr Phe Ser Trp Met
115 120 125

Gly Phe Ser Trp Thr Cys Arg Lys Arg Arg Lys His Tyr Gln Ser Tyr
130 135 140

Leu Arg Asn Gly Val Arg Ile Ser Val Asn Asp Phe Val Tyr Val Leu
145 150 155 160

Ala Glu Gln His Lys Arg Leu Val Ala Tyr Ile Glu Asp Leu Tyr Glu
165 170 175

Asp Ser Lys Gly Lys Lys Met Val Val Val Arg Trp Phe His Lys Thr
180 185 190

Glu Glu Val Gly Ser Val Leu Ser Asp Asp Asp Asn Asp Arg Glu Ile
195 200 205

Phe Phe Ser Leu Asn Arg Gln Asp Ile Ser Ile Glu Cys Ile Asp Tyr
210 215 220

Leu Ala Thr Val Leu Ser Pro Gln His Tyr Glu Lys Phe Leu Lys Val
225 230 235 240

Pro Met His Val Gln Thr Val Ala Phe Phe Cys Gln Lys Leu Tyr Gly
245 250 255

Asp Asp Gly Leu Lys Pro Tyr Asp Ile Thr Gln Leu Glu Gly Tyr Trp
260 265 270

Arg Gln Glu Met Leu Arg Tyr Leu Asn Val Ser Ile Leu Lys Ser Phe
275 280 285

Glu Gly Ala Gln Ala Pro Gly Thr Asp Pro Gly Leu Lys Ala Pro Leu
290 295 300

Val Gly Cys Val Gly Ile Arg Ser Arg Lys Arg Arg Arg Pro Ser Pro
305 310 315 320

Val Gly Thr Leu Asn Val Ser Tyr Ala Gly Asp Met Lys Gly Asp Cys
325 330 335

Lys Ser Ser Pro Asp Ser Val Leu Ala Val Thr Asp Ala Ser Ile Phe
340 345 350

Lys Gly Asp Glu Asp Gly Ser Ser His His Ile Lys Lys Gly Ser Leu
355 360 365

Ile Glu Val Leu Ser Glu Asp Ser Gly Ile Arg Gly Cys Trp Phe Lys
370 375 380

Ala Leu Val Leu Lys Lys His Lys Asp Lys Val Lys Val Gln Tyr Gln
385 390 395 400

Asp Ile Gln Asp Ala Asp Asp Glu Ser Lys Lys Leu Glu Glu Trp Ile
405 410 415

Leu Thr Ser Arg Val Ala Ala Gly Asp His Leu Gly Asp Leu Arg Ile
420 425 430

Lys Gly Arg Lys Val Val Arg Pro Met Leu Lys Pro Ser Lys Glu Asn
435 440 445

Asp Val Cys Val Ile Gly Val Gly Met Pro Val Asp Val Trp Trp Cys
450 455 460

Asp Gly Trp Trp Glu Gly Ile Val Val Gln Glu Val Ser Glu Glu Lys
465 470 475 480

Phe Glu Val Tyr Leu Pro Gly Glu Lys Lys Met Ser Ala Phe His Arg
485 490 495

Asn Asp Leu Arg Gln Ser Arg Glu Trp Leu Asp Asp Glu Trp Leu Asn
500 505 510

Ile Arg Ser Arg Ser Asp Ile Val Ser Ser Val Leu Ser Leu Thr Lys
515 520 525

Lys Lys Glu Met Glu Val Lys His Asp Glu Lys Ser Ser Asp Val Gly
530 535 540

Val Cys Asn Gly Arg Met Ser Pro Lys Thr Glu Ala Lys Arg Thr Ile
545 550 555 560

Ser Leu Pro Val Ala Thr Thr Lys Lys Ser Leu Pro Lys Arg Pro Ile
565 570 575

Pro Asp Leu Leu Lys Asp Val Leu Val Thr Ser Asp Leu Lys Trp Lys
580 585 590

Lys Ser Ser Arg Lys Arg Asn Arg Val Val Ser Cys Cys Pro His Asp
595 600 605

Pro Ser Leu Asn Asp Gly Phe Ser Ser Glu Arg Ser Leu Asp Cys Glu
610 615 620

Asn Cys Lys Phe Met Glu Asp Thr Phe Gly Ser Ser Asp Gly Gln His
625 630 635 640

Leu Thr Gly Thr Tyr Tyr Pro Asp Gly His Leu Leu Asn Ala Ile Leu
645 650 655

Gly Phe Lys Ile Thr Gly Asn Ser Gln Ala Phe Leu Gly Trp Ile Ile
660 665 670

Gly Leu Ala Arg Asn Gly Ile Gln Ile Arg Leu Cys Thr Tyr Val Val
675 680 685

Thr Val Gly His Ser Ala Leu Ile Gln Ser Ala Lys Phe Trp Met Gln
690 695 700

<210> 67

<211> 468

<212> PRT

<213> Arabidopsis thaliana

<400> 67

Met Gly Thr Gly Asn Ser Lys Glu Asn Trp Arg Gln Ser Ser Phe Arg
1 5 10 15

Ser Thr Ser Ala Ser Ser Ala Ser Pro Ser Ser Ser Ser Trp Ala Ser
20 25 30

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Gln Gln Ser Tyr Pro Gln Tyr Gly Ala Glu Ser Tyr Asn Tyr Pro Pro
        35                  40                  45

Pro Pro Ser Tyr Ala Gln Pro Pro Glu Tyr Thr Gln Pro Pro Pro Pro
    50                  55                  60

Leu Tyr Ser Thr Gln Pro Tyr Ser Ala Pro Ser Tyr Ser Ala Pro Pro
65                  70                  75                  80

Ser Gln Ser Tyr Gly Ser Asp Asn Lys Lys Arg Leu Glu Arg Lys Tyr
                85                  90                  95

Ser Lys Ile Ser Asp Asp Tyr Ser Ser Leu Glu Gln Val Thr Glu Ala
            100                 105                 110

Leu Ala Arg Ala Gly Leu Glu Ser Ser Asn Leu Ile Val Gly Ile Asp
        115                 120                 125

Phe Thr Lys Ser Asn Glu Trp Thr Gly Ala Arg Ser Phe Asn Arg Lys
    130                 135                 140

Ser Leu His Phe Ile Gly Ser Ser Pro Asn Pro Tyr Glu Gln Ala Ile
145                 150                 155                 160

Thr Ile Ile Gly Arg Thr Leu Ala Ala Phe Asp Glu Asp Asn Leu Ile
                165                 170                 175

Pro Cys Tyr Gly Phe Gly Asp Ala Ser Thr His Asp Gln Asp Val Phe
            180                 185                 190

Ser Phe Asn Ser Glu Asp Arg Phe Cys Asn Gly Phe Glu Glu Val Leu
        195                 200                 205

Ser Arg Tyr Lys Glu Ile Val Pro Gln Leu Lys Leu Ala Gly Pro Thr
    210                 215                 220

Ser Phe Ala Pro Ile Ile Asp Met Ala Met Thr Ile Val Glu Gln Ser
225                 230                 235                 240

Gly Gly Gln Tyr His Val Leu Val Ile Ile Ala Asp Gly Gln Val Thr
                245                 250                 255

Arg Ser Val Asp Thr Glu Asn Gly Gln Leu Ser Pro Gln Glu Gln Lys
            260                 265                 270

Thr Val Asp Ala Ile Val Gln Ala Ser Lys Leu Pro Leu Ser Ile Val
        275                 280                 285
```

Leu Val Gly Val Gly Asp Gly Pro Trp Asp Met Met Arg Glu Phe Asp
290 295 300

Asp Asn Ile Pro Ala Arg Ala Phe Asp Asp Phe Gln Phe Val Asn Phe
305 310 315 320

Thr Glu Ile Met Ala Lys Asn Lys Ala Gln Ser Leu Lys Glu Thr Glu
325 330 335

Phe Ala Leu Ser Ala Leu Met Glu Ile Pro Gln Gln Tyr Lys Ala Thr
340 345 350

Ile Glu Leu Asn Leu Leu Gly Arg Arg Asn Gly Tyr Ile Pro Glu Arg
355 360 365

Phe Pro Leu Pro Pro Pro Met Arg Gly Gly Ser Ser Ser Tyr Asn Ser
370 375 380

Pro Lys Pro Ser Arg Leu Pro Ser Phe Lys Pro Ser Val Pro Pro His
385 390 395 400

Pro Thr Glu Gly Tyr His Val Arg Ser Ser Pro Val Pro Pro Pro Thr
405 410 415

Ser Ser Ala Ser Asp Asn Gln Leu Cys Pro Ile Cys Leu Ser Asn Pro
420 425 430

Lys Asp Met Ala Phe Gly Cys Gly His Gln Thr Cys Cys Glu Cys Gly
435 440 445

Pro Asp Leu Gln Met Cys Pro Ile Cys Arg Ala Pro Ile Gln Thr Arg
450 455 460

Ile Lys Leu Tyr
465

<210> 68

<211> 390

<212> PRT

<213> Arabidopsis thaliana

<400> 68

Met Glu Met Thr Glu Ala Ser Lys Gln Thr Thr Ala Glu Gly Ser Ala
1 5 10 15

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Asn Pro Glu Pro Asp Gln Ile Leu Ser Pro Arg Arg Ser Leu Glu Leu
            20                  25                  30

Lys Gln Lys Lys Trp Trp Ile Ser Val Ser Leu Cys Ile Phe Leu Val
        35                  40                  45

Leu Leu Gly Asp Ser Leu Val Met Leu Leu Leu Asn Phe Phe Tyr Val
    50                  55                  60

Gln Asp Asn Arg Glu Asp Ser Asp Gln Asp Leu Gln Tyr Arg Gly Thr
65                  70                  75                  80

Trp Leu Gln Ala Leu Val Gln Asn Ala Ala Phe Pro Leu Leu Ile Pro
                85                  90                  95

Leu Phe Phe Ile Phe Pro Ser Pro Lys Gln Asn Gln Glu Thr Thr Asn
            100                 105                 110

Thr Arg Phe Leu Ser Phe Arg Leu Ile Leu Leu Tyr Ile Ser Leu Gly
        115                 120                 125

Val Leu Val Ala Ala His Ser Lys Leu Phe Ala Leu Gly Lys Leu Tyr
    130                 135                 140

Ala Asn Phe Gly Val Phe Thr Leu Ile Ser Ala Thr Gln Leu Ile Phe
145                 150                 155                 160

Thr Ala Ile Phe Ala Ala Ile Ile Asn Arg Phe Lys Phe Thr Arg Trp
                165                 170                 175

Ile Ile Leu Ser Ile Ile Gly Ser Ile Leu Ile Tyr Val Phe Gly Ser
            180                 185                 190

Pro Glu Phe Gly Gly Glu Pro Asp Glu Asn Glu Glu Phe Tyr Ser Ile
        195                 200                 205

Gln Ala Trp Leu Thr Phe Ala Ala Ser Val Ala Phe Ala Leu Ser Leu
    210                 215                 220

Cys Leu Phe Gln Leu Cys Phe Glu Lys Val Leu Val Lys Thr Lys Arg
225                 230                 235                 240

Tyr Gly Asn Lys Lys Val Phe Arg Met Val Ile Glu Met Gln Ile Cys
                245                 250                 255

Val Ser Phe Val Ala Thr Val Val Cys Leu Val Gly Leu Phe Ala Ser
            260                 265                 270
```

Gly Glu Asn Lys Glu Leu Gln Gly Asp Ser His Arg Phe Lys Lys Gly
275 280 285

Glu Thr Tyr Tyr Val Leu Ser Leu Ile Gly Leu Ala Leu Ser Trp Gln
290 295 300

Val Trp Ala Val Gly Leu Met Gly Leu Val Leu Tyr Val Ser Gly Val
305 310 315 320

Phe Gly Asp Val Val His Met Cys Thr Ser Pro Leu Val Ala Leu Phe
325 330 335

Val Val Leu Ala Phe Asp Phe Met Asp Asp Glu Phe Ser Trp Pro Arg
340 345 350

Ile Gly Thr Leu Ile Ala Thr Val Val Ala Leu Gly Ser Tyr Phe Tyr
355 360 365

Thr Leu His Lys Arg Asn Lys Lys Lys Met Val Glu Leu Tyr Gln Thr
370 375 380

Glu Asn Asn Ile Asp Val
385 390

<210> 69

<211> 275

<212> PRT

<213> Arabidopsis thaliana

<400> 69

Met Gln Leu Gly Ile Ser Ile Ile Arg Ser Ala Pro Asp Ala Ser Glu
1 5 10 15

Asp Asn Arg Ser Arg Gln Ser Arg Ser Ser Arg Thr Val Met Val His
20 25 30

Gln Pro Gly Phe Arg Ala Cys Leu Leu Arg Asn Gln Gly Asn Arg Asp
35 40 45

Leu Thr Ser Leu Ser Asp Cys Ile Ala Ala Arg Cys Asp Ser Leu Leu
50 55 60

Leu Gly Lys Ser His Ile Ile Asn Leu Ser Lys Asn Arg Arg Met Pro
65 70 75 80

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Phe Lys Ser Arg Glu Asn Thr Ile Phe Phe Ser Lys Arg Arg Lys Asn
85 90 95

Ser Ser Leu Cys Pro His Cys Thr Ala Pro Pro Phe Gln Leu Ser Pro
100 105 110

Thr Met Leu Leu Met Phe Cys His Asp Gly Ala Arg Leu Lys Gly Met
115 120 125

Asn Pro Arg Asn Ala Glu Glu Arg Lys Tyr Arg Gln Ala Glu Gly Leu
130 135 140

Val Thr Pro Gln Phe Leu Ser Ile Pro Gly Ser Pro Ile Asp Leu Thr
145 150 155 160

Lys Cys Trp Ser Ser Leu Leu Asn Ile Gln Gly Cys Lys Ile Glu Ile
165 170 175

Phe Lys Ser Val Phe Lys Trp Asn Val Leu Leu Ser Thr Gln Pro Leu
180 185 190

Leu His Thr Asn Glu Ser Asn Tyr Lys Thr Cys Gln Thr Ala Val Arg
195 200 205

Pro Pro Gln Gln Gly Arg Thr Glu Pro Ser Asn Asp Pro Leu Gln His
210 215 220

Arg Met Arg Pro Arg Thr Ile Val Ala Val Asn His Ala Leu Ala Ala
225 230 235 240

Arg Ser Trp Phe Ile Asn Gln Gly Glu Asp Gly Ala Ser Asp Gly Gly
245 250 255

Asn Glu Asn Asp Glu Asp Val Gly Met Leu Arg Asp Gly Gly Tyr Val
260 265 270

Ile Val Ser
275

<210> 70

<211> 459

<212> PRT

<213> Arabidopsis thaliana

<400> 70

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Met Asp Asn Gly Asp Ile Ala Cys Asp Gly Tyr His Lys Tyr Lys Glu
1               5                  10                  15

Asp Val Gln Leu Met Ala Glu Thr Gly Leu His Thr Phe Arg Phe Ser
            20                  25                  30

Ile Ser Trp Ser Arg Leu Ile Ser Asn Gly Arg Gly Ser Ile Asn Pro
        35                  40                  45

Lys Gly Leu Gln Phe Tyr Lys Asn Phe Ile Gln Glu Leu Val Lys His
    50                  55                  60

Gly Ile Glu Pro His Val Thr Leu His His Tyr Asp Phe Pro Gln Tyr
65                  70                  75                  80

Leu Glu Asp Asp Tyr Gly Gly Trp Thr Asn Arg Lys Ile Ile Lys Asp
                85                  90                  95

Phe Thr Ala Tyr Ala Asp Val Cys Phe Arg Glu Phe Gly Asn His Val
            100                 105                 110

Lys Phe Trp Thr Thr Ile Asn Glu Ala Asn Ile Phe Thr Ile Gly Gly
        115                 120                 125

Tyr Asn Asp Gly Asn Ser Pro Pro Gly Arg Cys Ser Phe Pro Gly Arg
    130                 135                 140

Asn Cys Thr Leu Gly Asn Ser Ser Thr Glu Thr Tyr Ile Val Gly His
145                 150                 155                 160

Asn Leu Leu Leu Ala His Ala Ser Val Ser Arg Leu Tyr Lys Gln Lys
                165                 170                 175

Tyr Lys Asp Ile Gln Gly Gly Ser Val Gly Phe Ser Leu Phe Ala Met
            180                 185                 190

Asn Phe Thr Pro Ser Thr Asn Ser Lys Asp Asp Glu Ile Ala Thr Lys
        195                 200                 205

Arg Ala Asn Asp Phe Tyr Leu Gly Trp Met Leu Glu Pro Leu Ile Tyr
    210                 215                 220

Gly Asp Tyr Pro Asp Val Met Lys Arg Thr Ile Gly Ser Arg Leu Pro
225                 230                 235                 240

Val Phe Ser Lys Glu Glu Ser Glu Gln Val Lys Gly Ser Ser Asp Phe
                245                 250                 255
```

```
Ile Gly Val Ile His Tyr Leu Thr Ala Leu Val Thr Asn Ile Asp Ile
            260                 265                 270

Asn Pro Ser Leu Ser Gly Ile Pro Asp Phe Asn Ser Asp Met Val Pro
        275                 280                 285

Asn Ile Leu Tyr Asn Phe Lys Tyr Ser Gln Ser Ile Phe Thr Ser Cys
    290                 295                 300

Gly Val Cys Phe Cys Leu Asp Lys Ser Val Val Ser Pro Trp Ala Met
305                 310                 315                 320

Glu Gly Ile Leu Glu Tyr Ile Lys Gln Ser Tyr Gly Asn Pro Pro Val
                325                 330                 335

Tyr Ile Leu Glu Asn Gly Lys Thr Met Asn Gln Asp Leu Glu Leu Gln
            340                 345                 350

Gln Lys Asp Thr Pro Arg Ile Glu Tyr Leu Asp Ala Tyr Ile Gly Ala
        355                 360                 365

Val Leu Lys Ala Val Arg Asn Lys Asp Met Thr Thr Cys Arg Asn Gly
    370                 375                 380

Ser Asp Thr Arg Gly Tyr Phe Val Trp Ser Phe Met Asp Leu Tyr Glu
385                 390                 395                 400

Leu Leu Asn Gly Tyr Lys Ser Ser Phe Gly Leu Tyr Ser Val Asn Phe
                405                 410                 415

Ser Asp Pro His Arg Lys Arg Ser Pro Lys Leu Ser Ala His Trp Tyr
            420                 425                 430

Ser Gly Phe Leu Lys Gly Lys Pro Thr Phe Leu Gly Ser Gln Gly Ile
        435                 440                 445

Thr Gln Leu His Ser Asn Phe Ser Ser Ser Arg
    450                 455
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<210> 71

<211> 173

<212> PRT

<213> Arabidopsis thaliana

<400> 71

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Met Gly Phe Arg Ala Leu Pro Leu Gln His Ser Ser Gly Phe Ile Ser
1 5 10 15

Thr Thr Lys Val Ser Ile Ser Arg Thr Ser Pro Arg Ile Phe Arg Asn
20 25 30

Pro Arg Trp Val Val Val Ser Ala Lys Gln Glu Lys Asp Glu Asp Lys
35 40 45

Lys Lys Asn Glu Glu Glu Thr Ser Leu Phe Thr Gln Leu Thr Asp Ala
50 55 60

Leu Asp Phe Ser Gln Val Arg Ser Glu Lys Asp Ala Glu Leu Leu Tyr
65 70 75 80

Glu Ala Arg Glu Ala Thr Lys Ser Gly Arg Lys Met Thr Gln Glu Gln
85 90 95

Tyr Gly Ala Leu Arg Arg Lys Ile Gly Gly Thr Tyr Lys Asp Phe Phe
100 105 110

Lys Ser Tyr Val Glu Val Asp Gly Gln Tyr Val Glu Glu Gly Trp Val
115 120 125

Asp Lys Thr Cys Lys Ile Cys Lys Lys Asp Thr Lys Gly Glu Ala Arg
130 135 140

Gln Val Asp Lys Leu Gly Arg Tyr Ala His Val Ser Cys Leu Gln Asn
145 150 155 160

Pro Pro Ser Gly Asn Phe Phe Thr Arg Leu Phe Ser Arg
165 170

<210> 72

<211> 442

<212> PRT

<213> Arabidopsis thaliana

<400> 72

Met Leu Lys Ile Lys Arg Val Pro Thr Val Val Ser Asn Tyr Gln Lys
1 5 10 15

Asp Asp Gly Ala Glu Asp Pro Val Gly Cys Gly Arg Asn Cys Leu Gly
20 25 30

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```
Ala Cys Cys Leu Asn Gly Ala Arg Leu Pro Leu Tyr Ala Cys Lys Asn
        35                  40                  45

Leu Val Lys Ser Gly Glu Lys Leu Val Ile Ser His Glu Ala Ile Glu
    50                  55                  60

Pro Pro Val Ala Phe Leu Glu Ser Leu Val Leu Gly Glu Trp Glu Asp
65                  70                  75                  80

Arg Phe Gln Arg Gly Leu Phe Arg Tyr Asp Val Thr Ala Cys Glu Thr
                85                  90                  95

Lys Val Ile Pro Gly Lys Tyr Gly Phe Val Ala Gln Leu Asn Glu Gly
            100                 105                 110

Arg His Leu Lys Lys Arg Pro Thr Glu Phe Arg Val Asp Lys Val Leu
        115                 120                 125

Gln Ser Phe Asp Gly Ser Lys Phe Asn Phe Thr Lys Val Gly Gln Glu
    130                 135                 140

Glu Leu Leu Phe Gln Phe Glu Ala Gly Glu Asp Ala Gln Val Gln Phe
145                 150                 155                 160

Phe Pro Cys Met Pro Ile Asp Pro Glu Asn Ser Pro Ser Val Val Ala
                165                 170                 175

Ile Asn Val Ser Pro Ile Glu Tyr Gly His Val Leu Leu Ile Pro Arg
            180                 185                 190

Val Leu Asp Cys Leu Pro Gln Arg Ile Asp His Lys Ser Leu Leu Leu
        195                 200                 205

Ala Val His Met Ala Ala Glu Ala Ala Asn Pro Tyr Phe Arg Leu Gly
    210                 215                 220

Tyr Asn Ser Leu Gly Ala Phe Ala Thr Ile Asn His Leu His Phe Gln
225                 230                 235                 240

Ala Tyr Tyr Leu Ala Met Pro Phe Pro Leu Glu Lys Ala Pro Thr Lys
                245                 250                 255

Lys Ile Thr Thr Thr Val Ser Gly Val Lys Ile Ser Glu Leu Leu Ser
            260                 265                 270

Tyr Pro Val Arg Ser Leu Leu Phe Glu Gly Gly Ser Ser Met Gln Glu
        275                 280                 285
```

Leu Ser Asp Thr Val Ser Asp Cys Cys Val Cys Leu Gln Asn Asn Asn
290 295 300

Ile Pro Phe Asn Ile Leu Ile Ser Asp Cys Gly Arg Gln Ile Phe Leu
305 310 315 320

Met Pro Gln Cys Tyr Ala Glu Lys Gln Ala Leu Gly Glu Val Ser Pro
325 330 335

Glu Val Leu Glu Thr Gln Val Asn Pro Ala Val Trp Glu Ile Ser Gly
340 345 350

His Met Val Leu Lys Arg Lys Glu Asp Tyr Glu Gly Ala Ser Glu Asp
355 360 365

Asn Ala Trp Arg Leu Leu Ala Glu Ala Ser Leu Ser Glu Glu Arg Phe
370 375 380

Lys Glu Val Thr Ala Leu Ala Phe Glu Ala Ile Gly Cys Ser Asn Gln
385 390 395 400

Glu Glu Asp Leu Glu Gly Thr Ile Val His Gln Gln Asn Ser Ser Gly
405 410 415

Asn Val Asn Gln Lys Ser Asn Arg Thr His Gly Gly Pro Ile Thr Asn
420 425 430

Gly Thr Ala Ala Glu Cys Leu Val Leu Gln
435 440

<210> 73

<211> 501

<212> PRT

<213> Arabidopsis thaliana

<400> 73

Met Asn Ser Glu Ser Leu Glu Asn Leu His Arg Pro Leu Ile Glu Ser
1 5 10 15

Ser Lys Ser Phe Val Asp Tyr Arg Leu Glu Thr Val Leu Thr Asp Arg
20 25 30

Glu Leu Pro Tyr Phe Arg Arg Ile Tyr Leu Ala Met Met Ile Glu Met
35 40 45

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```
Lys Phe Leu Phe His Leu Ala Ala Pro Ala Ile Phe Val Tyr Val Ile
 50                  55                  60

Asn Asn Gly Met Ser Ile Leu Thr Arg Ile Phe Ala Gly His Val Gly
65                  70                  75                  80

Ser Phe Glu Leu Ala Ala Ala Ser Leu Gly Asn Ser Gly Phe Asn Met
                85                  90                  95

Phe Thr Tyr Gly Leu Leu Leu Gly Met Gly Ser Ala Val Glu Thr Leu
            100                 105                 110

Cys Gly Gln Ala His Gly Ala His Arg Tyr Glu Met Leu Gly Val Tyr
        115                 120                 125

Leu Gln Arg Ser Thr Val Val Leu Ile Leu Thr Cys Leu Pro Met Ser
    130                 135                 140

Phe Leu Phe Leu Phe Ser Asn Pro Ile Leu Thr Ala Leu Gly Glu Pro
145                 150                 155                 160

Glu Gln Val Ala Thr Leu Ala Ser Val Phe Val Tyr Gly Met Ile Pro
                165                 170                 175

Val Ile Phe Ala Tyr Ala Val Asn Phe Pro Ile Gln Lys Phe Leu Gln
            180                 185                 190

Ser Gln Ser Ile Val Thr Pro Ser Ala Tyr Ile Ser Ala Ala Thr Leu
        195                 200                 205

Val Ile His Leu Ile Leu Ser Trp Ile Ala Val Tyr Arg Leu Gly Tyr
    210                 215                 220

Gly Leu Leu Ala Leu Ser Leu Ile His Ser Phe Ser Trp Trp Ile Ile
225                 230                 235                 240

Val Val Ala Gln Ile Val Tyr Ile Lys Met Ser Pro Arg Cys Arg Arg
                245                 250                 255

Thr Trp Glu Gly Phe Ser Trp Lys Ala Phe Glu Gly Leu Trp Asp Phe
            260                 265                 270

Phe Arg Leu Ser Ala Ala Ser Ala Val Met Leu Cys Leu Glu Ser Trp
        275                 280                 285

Tyr Ser Gln Ile Leu Val Leu Leu Ala Gly Leu Leu Lys Asn Pro Glu
    290                 295                 300
```

Leu Ala Leu Asp Ser Leu Ala Ile Cys Met Ser Ile Ser Ala Ile Ser
305 310 315 320

Phe Met Val Ser Val Gly Phe Asn Ala Ala Ala Ser Val Arg Val Ser
325 330 335

Asn Glu Leu Gly Ala Gly Asn Pro Arg Ala Ala Ala Phe Ser Thr Val
340 345 350

Val Thr Thr Gly Val Ser Phe Leu Leu Ser Val Phe Glu Ala Ile Val
355 360 365

Val Leu Ser Trp Arg His Val Ile Ser Tyr Ala Phe Thr Asp Ser Pro
370 375 380

Ala Val Ala Glu Ala Val Ala Asp Leu Ser Pro Phe Leu Ala Ile Thr
385 390 395 400

Ile Val Leu Asn Gly Ile Gln Pro Val Leu Ser Gly Val Ala Val Gly
405 410 415

Cys Gly Trp Gln Ala Phe Val Ala Tyr Val Asn Ile Gly Cys Tyr Tyr
420 425 430

Val Val Gly Ile Pro Val Gly Phe Val Leu Gly Phe Thr Tyr Asp Met
435 440 445

Gly Ala Lys Gly Ile Trp Thr Gly Met Ile Gly Gly Thr Leu Met Gln
450 455 460

Thr Ile Ile Leu Val Ile Val Thr Leu Arg Thr Asp Trp Asp Lys Glu
465 470 475 480

Val Glu Lys Ala Ser Ser Arg Leu Asp Gln Trp Glu Glu Ser Arg Glu
485 490 495

Pro Leu Leu Lys Gln
500

<210> 74

<211> 622

<212> PRT

<213> Arabidopsis thaliana

<400> 74

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Met Leu Glu Ala Ile Glu Arg Glu Phe Glu Ala Ala His Ala Gly Phe
1 5 10 15

Glu Gln Leu Lys Thr Asp Asp Ser Ala Gln Gly Leu Asp Asp Glu Gln
20 25 30

Ser Ala Lys Arg Gln Ser Met Leu Asp Glu Ile Glu Arg Asp Phe Glu
35 40 45

Ala Ala Thr Lys Gly Leu Glu Gln Leu Lys Ala Asp Asp Leu Thr Gly
50 55 60

Ile Asn Asp Glu Glu His Ala Ala Lys Arg Gln Lys Met Leu Glu Glu
65 70 75 80

Ile Glu Arg Glu Phe Glu Glu Ala Thr Lys Gly Leu Glu Glu Leu Arg
85 90 95

His Ser Thr Ser Ser Thr Asp Asp Glu Ala Gln Ser Ala Lys Arg Gln
100 105 110

Asn Met Leu Asp Glu Ile Glu Arg Glu Phe Glu Ala Ala Thr Ser Gly
115 120 125

Leu Lys Glu Leu Lys Ile Asn Ala His Thr Val Lys Asp Asp Val Asp
130 135 140

Asp Lys Glu Gln Asp Ala Lys Arg Gln Ser Met Leu Asp Ala Ile Glu
145 150 155 160

Arg Glu Phe Glu Ala Val Thr Glu Ser Phe Lys Gln Leu Glu Asp Ile
165 170 175

Ala Asp Asn Lys Ala Glu Gly Asp Asp Glu Ser Ala Lys Arg Gln Ser
180 185 190

Met Leu Asp Glu Ile Glu Arg Glu Phe Glu Ala Ala Thr Asn Ser Leu
195 200 205

Lys Gln Leu Asn Leu Asp Asp Phe Ser Glu Gly Asp Asp Ser Ala Glu
210 215 220

Ser Ala Arg Arg Asn Ser Met Leu Glu Ala Ile Glu Arg Glu Phe Glu
225 230 235 240

Ala Ala Thr Lys Gly Leu Glu Glu Leu Lys Ala Asn Asp Ser Thr Gly
245 250 255

```
Asp Lys Asp Asp Asp Glu His Val Ala Arg Arg Lys Ile Met Leu Glu
            260                 265                 270

Ala Ile Glu Arg Glu Phe Glu Ala Ala Thr Lys Gly Leu Glu Glu Leu
        275                 280                 285

Lys Asn Glu Ser Glu Gln Ala Glu Asn Lys Arg Asn Ser Met Leu Glu
    290                 295                 300

Ala Phe Glu Arg Glu Phe Glu Ala Ala Thr Asn Ala Lys Ala Asn Gly
305                 310                 315                 320

Glu Asn Ser Ala Lys Asn Pro Ser Thr Ile Ser Thr Thr Val Gln Lys
                325                 330                 335

Ser Ser Gly Gly Tyr Asn Ala Gly Leu Glu Gly Leu Leu Lys Pro Ala
            340                 345                 350

Asp Gly Val Cys Gly Cys Phe Asn Lys Asp Lys Asp Gly Leu Gln Ala
        355                 360                 365

Asp Thr Asp Ser Ser Ile Asn Ile Ala Glu Ile Leu Ala Glu Glu Ser
    370                 375                 380

Lys Leu Gln Gly Ser Gly Thr Ser Arg Leu Thr Thr Ser Leu Asn Asn
385                 390                 395                 400

Leu Val Asp Thr His Arg Lys Glu Thr Ser Ser Lys Val Gly Ser Val
                405                 410                 415

Leu Gly Ser Ser Ser Ser Val Thr Ser Thr Thr Ser Glu Ser Ala Ala
            420                 425                 430

Thr Ser Glu Ser Ile Glu Ser Leu Lys Gln Thr Leu Arg Lys Leu Arg
        435                 440                 445

Gly Leu Ser Ala Arg Asp Leu Val Asn His Pro Asn Phe Asp Ala Ile
    450                 455                 460

Ile Ala Ala Gly Thr Arg Tyr Glu Val Leu Ser Ser Ala Ser Ile Gly
465                 470                 475                 480

Tyr Ile Ser Leu Leu Ala Lys Tyr Lys Thr Val Ile Lys Glu Gly Leu
                485                 490                 495

Glu Ala Ser Gln Arg Val Gln Ile Ala Gln Thr Arg Ala Lys Leu Leu
            500                 505                 510
```

Lys Glu Thr Ala Met Glu Lys Gln Arg Thr Val Asp Ser Val Phe Ala
515 520 525

Ala Ala Lys Thr Thr Ala Gln Arg Gly Asp Ala Leu His Ile Arg Ile
530 535 540

Val Ala Ile Lys Lys Leu Leu Ala Lys Leu Glu Ala Glu Lys Val Asp
545 550 555 560

Val Asp Ser Lys Phe Thr Ser Leu Thr Thr Ser Leu Ser Glu Leu Leu
565 570 575

Lys Glu Ala Ser Gln Ala Tyr Glu Glu Tyr His Glu Ala Val His Lys
580 585 590

Ala Lys Asp Glu Gln Ala Ala Glu Glu Phe Ala Val Glu Thr Thr Lys
595 600 605

Arg Ala Glu His Ile Trp Val Glu Phe Leu Ser Ser Leu Asn
610 615 620

<210> 75

<211> 86

<212> PRT

<213> Arabidopsis thaliana

<400> 75

Met Glu Ser Ser Leu Gly Phe Met Ala Val Phe Ala Val Ser Gly Ser
1 5 10 15

Val Val Phe Leu Ala Ser Gln Phe His Lys Arg Leu Leu Ser Asp Tyr
20 25 30

Met Asp Lys Phe Glu Phe Glu Ile Arg Ala Gln Lys Lys Met Val Met
35 40 45

Lys Lys Lys Val Arg Phe Ala Ala Asp Val Val Glu Pro Ser Gly Asn
50 55 60

Asn Lys Glu Tyr Arg Arg Arg His Ser Ser Lys Ala Lys Ser Asn Ser
65 70 75 80

Lys Met Ala Ala Thr Ile
85

<210> 76

<211> 418

<212> PRT

<213> Arabidopsis thaliana

<400> 76

Met Ile Lys Leu Cys Phe Met Thr Ser His Gly Tyr Ser Ile Pro Gly
1 5 10 15

Leu Gly Leu Pro Gln Asp Leu Cys Asn Thr Glu Ile Ile Lys Asn Ser
20 25 30

Arg Ser His Leu Val Asn Pro Gly Ala Arg Gln Glu Ile Ile Pro Ala
35 40 45

Ser Ser Phe Asn Leu Asn Thr Glu Leu Leu Glu Pro Trp Lys Pro Val
50 55 60

Ser Ser Phe Ser Gln Phe Val Glu Ile Asp Ser Ala Met Met Lys Pro
65 70 75 80

Leu Leu Met Asp Val His Glu Thr Ala Pro Glu Ser Leu Ile Leu Ser
85 90 95

Phe Gly Ile Ala Asp Lys Phe Ala Arg Gln Glu Lys Val Met Glu Phe
100 105 110

Leu Leu Ser Gln Ser Glu Glu Phe Lys Glu Lys Gly Phe Asp Met Ser
115 120 125

Leu Leu Asn Glu Leu Met Glu Phe Glu Ser Met Lys Ser Ser Ser Gln
130 135 140

Leu Arg Pro Tyr Asp Thr Ser Ser Val Leu Tyr Leu Asn Gln Glu Leu
145 150 155 160

Gly Lys Pro Val Leu Asp Leu Val Arg Asp Met Met Glu Asn Pro Glu
165 170 175

Phe Ser Val Arg Ser Asn Gly His Val Leu Phe Ser Ser Ser Ser Asn
180 185 190

Pro Glu Leu Asn Asp Leu Leu Ser Ile Ala Ser Glu Phe Asn Leu Ser
195 200 205

Arg Asn Ser Thr Thr Lys Trp Arg Gln Leu Ser Pro Leu Ile Pro His
210 215 220

Phe Gln Arg Phe Glu Ser Asp Val Phe Thr Pro Ala Lys Leu Lys Ala
225 230 235 240

Val Thr Val Leu Ala Pro Leu Lys Ser Pro Glu Lys Ser Arg Leu Lys
245 250 255

Ser Pro Arg Lys His Asn Thr Lys Arg Lys Ala Lys Glu Arg Asp Leu
260 265 270

Tyr Lys Arg Asn His Leu His Ala Tyr Glu Ser Leu Leu Ser Leu Met
275 280 285

Ile Gly Asn Asp His Arg His Lys His Thr Thr Val Leu Ser Leu Gln
290 295 300

Lys Ser Cys Gly Glu Leu Ser Glu Leu Leu Thr Gln Phe Ser Ile Thr
305 310 315 320

Ala Ala Gly Thr Gly Ile Ala Val Leu Phe Ser Val Val Cys Ser Leu
325 330 335

Ala Ser Arg Arg Val Pro Phe Cys Ala Asn Lys Phe Phe Asp Thr Gly
340 345 350

Leu Gly Leu Ser Leu Val Ile Leu Ser Trp Ala Val Asn Arg Leu Arg
355 360 365

Glu Val Ile Val His Val Asn Arg Lys Ala Asn Lys Pro Cys Ser Ser
370 375 380

Leu Lys Asp Asp Glu Ile Ile Asn Ser Val Glu Arg Ser Met Lys Glu
385 390 395 400

Val Tyr Tyr Arg Ala Ala Thr Val Ile Ala Val Phe Ala Leu Arg Phe
405 410 415

Ala Cys

<210> 77

<211> 72

<212> PRT

<213> Arabidopsis thaliana

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<400> 77

Met Ala Ser Ile Cys Glu Asp Pro Gly Lys Ser Ser Trp Pro Glu Leu
1 5 10 15

Leu Gly Ala Lys Gly Glu Asp Ala Lys Glu Val Ile Glu Arg Glu Asn
20 25 30

Pro Lys Met Lys Ala Val Ile Ile Leu Asp Gly Thr Val Val Pro Glu
35 40 45

Ile Phe Ile Cys Ser Arg Val Tyr Val Trp Val Asn Asp Cys Gly Ile
50 55 60

Val Val Gln Ile Pro Ile Ile Gly
65 70

<210> 78

<211> 191

<212> PRT

<213> Arabidopsis thaliana

<400> 78

Met Ser Arg Cys Gly Ser Leu Gly Leu Tyr Ala Pro Asn Ala Leu Pro
1 5 10 15

Ser Leu Ser Leu Lys Pro Arg Ser Val Lys Ser Pro Phe Cys Ile Thr
20 25 30

Ser His Thr Lys Pro Asn Asp Thr Leu Leu His Asn Val Asn Lys Met
35 40 45

Arg Ala Lys Ala Cys Asp Ile Leu Gly Ala Lys Lys Thr Ile Leu Ala
50 55 60

Ala Gln Leu Gly Ala Val Leu Ala Thr Ile Asp His Pro Ala Leu Ala
65 70 75 80

Ile Thr Gly Val Asn Asn Gln Gln Glu Leu Ser Ser Val Val Leu Asp
85 90 95

Ile Gly Ile Ile Ser Val Trp Tyr Phe Leu Val Met Pro Pro Ile Ile
100 105 110

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Met Asn Trp Leu Arg Val Arg Trp Tyr Arg Arg Lys Phe Phe Glu Met
115 120 125

Tyr Leu Gln Phe Met Phe Val Phe Met Phe Phe Pro Gly Leu Leu Leu
130 135 140

Trp Ala Pro Phe Leu Asn Phe Arg Lys Phe Pro Arg Asp Pro Asn Met
145 150 155 160

Lys Asn Pro Trp Asp Lys Pro Thr Asp Pro Asp Ser Ile Lys Asn Val
165 170 175

Tyr Leu Lys Tyr Pro Tyr Ala Thr Pro Glu Asp Tyr Asp Leu Asp
180 185 190

<210> 79

<211> 212

<212> PRT

<213> Arabidopsis thaliana

<400> 79

Met Ala Thr Val Thr Ile Leu Ser Pro Lys Ser Ile Pro Lys Val Thr
1 5 10 15

Asp Ser Lys Phe Gly Ala Arg Val Ser Asp Gln Ile Val Asn Val Val
20 25 30

Lys Cys Gly Lys Ser Gly Arg Arg Leu Lys Leu Ala Lys Leu Val Ser
35 40 45

Ala Ala Gly Leu Ser Gln Ile Glu Pro Asp Ile Asn Glu Asp Pro Ile
50 55 60

Gly Gln Phe Glu Thr Asn Ser Ile Glu Met Glu Asp Phe Lys Tyr Gly
65 70 75 80

Tyr Tyr Asp Gly Ala His Thr Tyr Tyr Glu Gly Glu Val Gln Lys Gly
85 90 95

Thr Phe Trp Gly Ala Ile Ala Asp Asp Ile Ala Ala Val Asp Gln Thr
100 105 110

Asn Gly Phe Gln Gly Leu Ile Ser Cys Met Phe Leu Pro Ala Ile Ala
115 120 125

Leu Gly Met Tyr Phe Asp Ala Pro Gly Glu Tyr Leu Phe Ile Gly Ala
130 135 140

Ala Leu Phe Thr Val Val Phe Cys Ile Ile Glu Met Asp Lys Pro Asp
145 150 155 160

Gln Pro His Asn Phe Glu Pro Gln Ile Tyr Lys Leu Glu Arg Gly Ala
165 170 175

Arg Asp Lys Leu Ile Asn Asp Tyr Asn Thr Met Ser Ile Trp Asp Phe
180 185 190

Asn Asp Lys Tyr Gly Asp Val Trp Asp Phe Thr Ile Glu Lys Asp Asp
195 200 205

Ile Ala Thr Arg
210

<210> 80

<211> 214

<212> PRT

<213> Arabidopsis thaliana

<400> 80

Met Ala Thr Arg Gly Ala Val Ala Ala Ala Ala Ser Thr Ile Trp Lys
1 5 10 15

His Arg Arg Asn Pro Ser Leu Arg Ser Leu Ser Arg His Phe Asn Pro
20 25 30

Asn Phe Asn His Arg Ile Ile Pro Thr Gly Phe Lys Tyr Gln Val Arg
35 40 45

Ala Ile Gln Gly Thr Ser Thr Asp Pro Val Ile Thr Pro Leu Lys Asn
50 55 60

Arg Glu Glu Pro Lys Pro Gln Asn Trp Lys Ile Lys Met Leu Tyr Asp
65 70 75 80

Gly Asp Cys Pro Leu Cys Met Arg Glu Val Asn Met Leu Met Glu Arg
85 90 95

Asn Glu Lys His Gly Thr Ile Lys Phe Val Asp Ile Ser Ser Asn Asp
100 105 110

Tyr Ser Pro Glu Asp Asn Gln Gly Leu Asp Tyr Lys Thr Val Met Gly
115 120 125

Gln Ile His Ala Ile Gln Ser Asp Gly Asn Val Val Lys Gly Val Glu
130 135 140

Ala Phe Arg Arg Leu Tyr Glu Glu Val Gly Leu Gly Trp Val Tyr Thr
145 150 155 160

Ile Thr Lys Phe Glu Pro Ile Gly Lys Leu Ala Asp Val Val Tyr Asp
165 170 175

Val Trp Ala Lys Tyr Arg Leu Gln Val Thr Gly Arg Pro Ser Ile Glu
180 185 190

Ala Ile Leu Glu Ala Arg Lys Lys Asp Lys Val Glu Thr Cys Gly Glu
195 200 205

Ser Lys Asn Cys Lys Ile
210

<210> 81

<211> 158

<212> PRT

<213> Arabidopsis thaliana

<400> 81

Met Ala Phe Ser Ala Thr Val Ser Gln Leu Ser Ser Leu Ser Thr Ile
1 5 10 15

Ser Ser Ser Leu Pro Ile Ser Ser Arg Arg Leu Pro His Arg Ser Leu
20 25 30

Pro Gln Phe Thr Val Lys Ala Glu Ala Glu Lys Glu Lys Gln Ser Thr
35 40 45

Gln Gly Lys Ser Asp Gly Glu Ala Ser Pro Ala Ala Thr Lys Thr Pro
50 55 60

Lys Thr Leu Pro Lys Lys Pro Val Tyr Ser Met Lys Lys Gly Gln Ile
65 70 75 80

Val Arg Val Glu Lys Glu Lys Tyr Leu Asn Ser Ile Asn Tyr Leu Ser
85 90 95

Val Gly His Pro Pro Phe Tyr Lys Gly Leu Asp Tyr Ile Tyr Glu Asp
100 105 110

Arg Gly Glu Val Leu Asp Leu Arg Val Phe Glu Thr Gly Glu Tyr Ala
115 120 125

Leu Val Gly Trp Val Gly Ile Pro Thr Ala Pro Ala Trp Leu Pro Thr
130 135 140

Asp Met Leu Ile Lys Cys Glu Lys Leu Val Tyr Glu Arg Met
145 150 155

<210> 82

<211> 704

<212> PRT

<213> Arabidopsis thaliana

<400> 82

Met Glu Thr Asn Gln Trp Arg Ser Arg Lys Lys Ile Glu Ser Ala Ala
1 5 10 15

Glu Thr Leu Gln Val Ser Ser Arg Arg Gly Arg Gly Gln Ala Arg Met
20 25 30

Val Pro Pro Val Ser Gly Val Arg Ser Glu Arg Ala Arg Lys Ser Leu
35 40 45

Ser Glu Lys Leu Glu Thr Val Ala Leu Asn Ser Pro Lys Lys Asp Ala
50 55 60

Arg Val Ser Leu Tyr Gly Glu Lys Ser Val Val Asp Glu Ile Phe Leu
65 70 75 80

Glu Asp Glu Glu Met Gly His Glu Thr Gly Leu Lys Asn Gly Glu Ser
85 90 95

Ser Pro Phe Cys Gly Val Ser Asp Lys Leu Leu Gln Arg Ile Glu Leu
100 105 110

Leu Gly Arg Asp His Glu Ala Thr Arg Leu Asp Asn Asn Lys Phe Arg
115 120 125

Ser Ile Glu Ser Met Lys Lys Arg Gln Glu Glu Ser Ala Cys Asp Asp
130 135 140

Leu Val Asp Met Lys Thr Lys Ile Gln Thr Leu Ala Ala Glu Asn Thr
145 150 155 160

Gln Leu Lys Lys Ser Leu Val Ala Lys Glu Glu Leu Ala Val Ser Leu
165 170 175

Gln Glu Arg Lys Phe Gln Val Glu Ser Glu Phe Glu Ala Leu Met Thr
180 185 190

Arg Leu Asp Ser Thr Glu Lys Glu Asn Ala Phe Leu Arg Tyr Glu Tyr
195 200 205

Thr Val Leu Glu Lys Asp Leu Gln Val Lys Thr Glu Glu Thr Glu His
210 215 220

Thr Arg Arg Ser Met Glu Leu Thr His Lys Gln Gln Leu Arg Asn Val
225 230 235 240

Asn Lys Ile Val Glu Leu Glu Ala Glu Cys Gln Arg Leu Arg Leu Leu
245 250 255

Phe Arg Lys Lys Phe Pro Glu Lys Ser Ile Ser Met Arg Asn Glu Gly
260 265 270

Glu Glu Lys Lys Met Glu Met Arg Arg Arg Asn Ala Asn Lys Ser Asp
275 280 285

Met Met Met Arg Asp Glu Val Gln Ser Arg Lys Leu Lys Tyr Asp Leu
290 295 300

Leu Met Glu Gln Ile Gly Asn Val Arg Ala Glu Asn Lys Asn Leu Met
305 310 315 320

Asp Ile Ile Met Lys Lys Asn Ile Glu Ile Lys Asp Leu Ser Arg Gly
325 330 335

Gln Lys Pro Leu Glu Ala Ser Ser Phe Asp Ile Gln Ser Glu Ser Ser
340 345 350

Val Met Ser Pro Cys Gly Ser Lys Glu Met Lys Leu Leu Met Asp Asp
355 360 365

Phe Asn Glu Met Glu Lys Leu Ala Ile Val Cys Thr Glu Lys Asp Pro
370 375 380

Arg Val Asp Asp Glu Lys Glu Gly Ser Phe Asp Trp Ile Gln Val Val
385 390 395 400

Leu Ser Ala Ile Thr Lys Gln Glu Arg Ile Ser Lys Arg Gly Val Lys
405 410 415

Glu Leu Leu Gln Asp Ile Lys Ile Ala Leu Gly Cys Met Asp Glu Asn
420 425 430

Asp Asn Val Glu Arg Lys Lys Gly Glu Glu Asp Pro Leu Cys Ile Thr
435 440 445

Trp Lys Ser Asn Asn Glu Ser Gly Pro Met Thr Lys Asp Glu Ile Lys
450 455 460

Arg His Leu Gly Leu Thr Lys Ser Asp Lys Val Glu Lys Ile Glu Ser
465 470 475 480

Asp Glu Lys Gln Glu Leu Arg Lys Lys Leu Glu Glu Ser Val Glu Lys
485 490 495

Ile Arg Asn Leu Glu Ala Glu Met Lys Thr Leu Arg Glu Asn Lys Glu
500 505 510

Lys Val Glu Ala Glu Met Glu Thr Glu Lys Ser Met Lys Glu Asp Leu
515 520 525

Asp Thr Lys Leu Asn Ile Thr Arg Ala Asn Leu Asn Glu Thr Gln Lys
530 535 540

Lys Leu Ser Ser Leu Glu Val Glu Phe Asp Tyr Arg Lys Ser Cys Cys
545 550 555 560

Glu Glu Leu Glu Gly Thr Cys Ile Glu Leu Gln Leu Gln Leu Glu Ser
565 570 575

Val Glu Thr Lys Lys Pro Thr Gln Arg Asn Lys Asn Gly Trp Asp Ile
580 585 590

Ala Thr Ala Ser Val Lys Leu Ser Glu Cys Gln Glu Thr Ile Thr Ser
595 600 605

Leu Arg Lys Gln Leu Arg Ala Leu Ser Thr Thr Glu Thr Ser Ser Thr
610 615 620

Ile Lys Phe Leu His Lys Arg Ser Ser Leu Arg Glu Asn Ile Ala Glu
625 630 635 640

Asp Asp Thr Asn Arg Val Ala Gln Asp Asp Asp Gly Asn Arg Tyr Asn
645 650 655

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Ala Leu Ile Val Tyr Glu Pro Val Lys Ala Arg Gly Glu Lys Met Glu
660 665 670

Met Val Pro Arg Lys Lys Gln Gly Leu Gly Phe Leu Lys Lys Leu Leu
675 680 685

Phe Arg Arg Lys Arg Val Ser Ser Lys Lys Cys Leu Ala Leu Thr Met
690 695 700

<210> 83

<211> 559

<212> PRT

<213> Arabidopsis thaliana

<400> 83

Met Asp Leu Gly Arg Lys Pro Leu Ala Arg Phe Pro Ser Gly Asp Trp
1 5 10 15

Val Ile Ser Glu Gln Pro Val Thr His Gln Asp Leu Glu Leu Ala Val
20 25 30

Ser Lys Val Gly Asp Phe Ser Asp Asp Asn Arg Ser Gly Ile Asp Arg
35 40 45

Ser Leu His Arg Ile Ser Ala Ile Arg Asn Arg Lys Leu Gln Val Ile
50 55 60

Gly Leu Thr Cys Arg Val Gly Arg Val Val Ser Gly Ser Ala Glu Ile
65 70 75 80

Ile Arg Asp Leu Ile Glu Gly Gly Gly Ser Ile Leu Val Ile Gly Ser
85 90 95

Pro Gly Val Gly Lys Thr Thr Leu Ile Arg Glu Ile Ala Arg Met Leu
100 105 110

Ala Asp Glu His Arg Lys Arg Val Val Ile Val Asp Thr Ser Asn Glu
115 120 125

Ile Gly Gly Asp Gly Asp Val Pro His Ser Gly Ile Gly Arg Ala Arg
130 135 140

Arg Met Gln Val Pro Asn Val Asn Leu Gln His Asp Val Met Ile Glu
145 150 155 160

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```
Ala Val Glu Asn His Met Pro Glu Thr Ile Ile Ile Asp Glu Ile Gly
                165                 170                 175

Thr Glu Leu Glu Ala Leu Ala Ala Ser Thr Ile Ala Gln Arg Gly Val
            180                 185                 190

Gln Leu Val Ala Thr Ala His Gly Met Thr Ile Asp Asn Ile Ile Lys
        195                 200                 205

Asn Pro Ser Leu Gln Ile Leu Ile Gly Gly Ile Glu Ser Val Thr Leu
    210                 215                 220

Gly Asp Glu Glu Ala Arg Lys Arg Lys Val Gln Lys Thr Ile Leu Glu
225                 230                 235                 240

Arg Lys Gly Pro Pro Thr Phe Thr Cys Ala Val Glu Met Ile Ser Arg
                245                 250                 255

Thr Glu Cys Arg Val His Gln Arg Leu Asp Val Thr Val Asp Ala Ile
            260                 265                 270

Leu Ala Gly Lys Ser Ala Pro Phe Glu Ile Arg Gln Ile Arg Gly Glu
        275                 280                 285

Asp Asp Val Pro His Lys Leu Val Thr Pro Ile Pro Leu Glu Asn Leu
    290                 295                 300

Glu Glu Glu Pro Ala Pro Leu Leu Asn Arg Asp Phe Val Ser Glu Leu
305                 310                 315                 320

Leu Ser Asp Asp Glu Asp Glu Asp Phe Leu Leu Ile Arg Ser Asn Lys
                325                 330                 335

Ala Arg Ser Asn Thr Tyr Thr Ser Pro Arg Ser Ser Pro Val His Val
            340                 345                 350

Tyr Thr Tyr Asn Val Leu Glu Ala Asp Leu Leu Gln Val Ala Glu Val
        355                 360                 365

Met Gly Leu Asp Asp Glu Ile Glu Val Thr Asp Asp Val Gly Glu Ala
    370                 375                 380

Asp Val Ile Leu Ala Ser Ser Ser Glu Leu Lys Gln Asn Ser Ser Ile
385                 390                 395                 400

Arg Arg Val Ala Lys Leu His Lys Leu Pro Ile Phe Val Ile Lys Ser
                405                 410                 415
```

Thr Thr Met Ala Gln Met Val Lys Ala Val Arg Met Ile Leu Gly Arg
420 425 430

Glu Ser Phe Gly Ser Ala Pro Lys Ala Ile Glu Lys Ser Ser Val Asp
435 440 445

Asp Ile Glu Ile Lys Asp Asp Ala Pro Glu Ser Lys Pro Ser Leu Glu
450 455 460

Glu Leu Asp Ala Leu Glu Glu Val Arg Leu Ala Ile Glu Tyr Ile Val
465 470 475 480

Ile Pro Gly Gly Glu Pro Val Glu Leu Leu Pro Arg Arg Ser Asp Ile
485 490 495

Ile Val Arg Gln Leu Glu Leu Val Glu Ser Tyr Gln Leu Ala Val Glu
500 505 510

Asn Leu Gly Thr His Leu Asn Pro Arg Leu Gln Ile Leu Pro Arg Arg
515 520 525

Ser Thr Lys Lys Thr Leu Thr Ser Ser Ser Pro Gln Lys Ser Ala Asp
530 535 540

Gly Ser Met Gly Thr Thr Gly Thr Arg Leu Pro Phe Leu Lys Asp
545 550 555

<210> 84

<211> 326

<212> PRT

<213> Arabidopsis thaliana

<400> 84

Met Ala Val Ala Ser Leu Ser Ile Cys Phe Ser Ala Arg Pro His Leu
1 5 10 15

Leu Leu Arg Asn Phe Ser Pro Arg Pro Lys Phe Val Ala Met Ala Ala
20 25 30

Met Ser Glu Asp Pro Ile Arg Glu Trp Ile Leu Thr Glu Gly Lys Ala
35 40 45

Thr Gln Ile Thr Lys Ile Gly Ser Val Gly Gly Gly Cys Ile Asn Leu
50 55 60

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```
Ala Ser His Tyr Gln Thr Asp Ala Gly Ser Phe Phe Val Lys Thr Asn
65                  70                  75                  80

Arg Ser Ile Gly Pro Ala Met Phe Glu Gly Glu Ala Leu Gly Leu Glu
                85                  90                  95

Ala Met Tyr Glu Thr Arg Thr Ile Arg Val Pro Asn Pro His Lys Ala
            100                 105                 110

Gly Glu Leu Pro Thr Gly Gly Ser Tyr Ile Ile Met Glu Phe Ile Asp
        115                 120                 125

Phe Gly Gly Ser Arg Gly Asn Gln Ala Glu Leu Gly Arg Lys Leu Ala
    130                 135                 140

Glu Met His Lys Ala Gly Lys Thr Ser Lys Gly Phe Gly Phe Glu Val
145                 150                 155                 160

Asp Asn Thr Ile Gly Ser Thr Pro Gln Ile Asn Thr Trp Ser Ser Asp
                165                 170                 175

Trp Ile Glu Phe Tyr Gly Glu Lys Arg Leu Gly Tyr Gln Leu Lys Leu
            180                 185                 190

Ala Arg Asp Gln Tyr Gly Asp Ser Ala Ile Tyr Gln Lys Gly His Thr
        195                 200                 205

Leu Ile Gln Asn Met Ala Pro Leu Phe Glu Asn Val Val Ile Glu Pro
    210                 215                 220

Cys Leu Leu His Gly Asp Leu Trp Ser Gly Asn Ile Ala Tyr Asp Lys
225                 230                 235                 240

Asn Asn Glu Pro Val Ile Leu Asp Pro Ala Cys Tyr Tyr Gly His Asn
                245                 250                 255

Glu Ala Asp Phe Gly Met Ser Trp Cys Ala Gly Phe Gly Glu Ser Phe
            260                 265                 270

Tyr Asn Ala Tyr Phe Lys Val Met Pro Lys Gln Ala Gly Tyr Glu Lys
        275                 280                 285

Arg Arg Asp Leu Tyr Leu Leu Tyr His Tyr Leu Asn His Tyr Asn Leu
    290                 295                 300

Phe Gly Ser Gly Tyr Arg Ser Ser Ala Met Ser Ile Ile Asp Asp Tyr
305                 310                 315                 320
```

Leu Arg Met Leu Lys Ala
325

<210> 85

<211> 78

<212> PRT

<213> Arabidopsis thaliana

<400> 85

Met Leu Asp Thr Leu Ile Gly Gly Ile Val Gly Gly Ile Ala Gly Ala
1 5 10 15

Ile Ile Gly Thr Val Asp Gly Phe Ala Arg Gly Ile Gly Ile Cys Pro
20 25 30

Asp Ser Tyr Gln Ser Cys Thr Arg Thr Asp Cys Glu Glu His Lys Lys
35 40 45

Lys Leu Pro Thr Asn Leu Ser Arg Asn Gly Gly Ala Ala Ala Val Lys
50 55 60

Ala Lys Glu Asn Gly Arg Arg Arg Arg Gln Lys Asp Arg Glu
65 70 75

<210> 86

<211> 306

<212> PRT

<213> Arabidopsis thaliana

<400> 86

Met Ala Ala Ala Ser Leu His Thr Ser Ile Ser Pro Arg Ser Phe Leu
1 5 10 15

Pro Leu Ser Lys Pro Ser Leu Lys Pro His Arg Ser Gln Ile Leu Leu
20 25 30

Arg Asn Lys Gln Arg Asn Cys Val Ser Cys Ala Leu Ile Arg Asp Glu
35 40 45

Ile Asp Leu Ile Pro Val Gln Ser Arg Asp Arg Thr Asp His Glu Glu
50 55 60

Gly Ser Val Val Val Met Ser Thr Glu Thr Ala Val Asp Gly Asn Glu
65 70 75 80

Ser Val Val Val Gly Phe Ser Ala Ala Thr Ser Glu Gly Gln Leu Ser
85 90 95

Leu Glu Gly Phe Pro Ser Ser Ser Ser Ser Gly Ala Asp Leu Gly Asp
100 105 110

Glu Lys Arg Arg Glu Asn Glu Glu Met Glu Lys Met Ile Asp Arg Thr
115 120 125

Ile Asn Ala Thr Ile Val Leu Ala Ala Gly Ser Tyr Ala Ile Thr Lys
130 135 140

Leu Leu Thr Ile Asp His Asp Tyr Trp His Gly Trp Thr Leu Phe Glu
145 150 155 160

Ile Leu Arg Tyr Ala Pro Gln His Asn Trp Ile Ala Tyr Glu Glu Ala
165 170 175

Leu Lys Gln Asn Pro Val Leu Ala Lys Met Val Ile Ser Gly Val Val
180 185 190

Tyr Ser Val Gly Asp Trp Ile Ala Gln Cys Tyr Glu Gly Lys Pro Leu
195 200 205

Phe Glu Ile Asp Arg Ala Arg Thr Leu Arg Ser Gly Leu Val Gly Phe
210 215 220

Thr Leu His Gly Ser Leu Ser His Phe Tyr Tyr Gln Phe Cys Glu Glu
225 230 235 240

Leu Phe Pro Phe Gln Asp Trp Trp Val Val Pro Val Lys Val Ala Phe
245 250 255

Asp Gln Thr Val Trp Ser Ala Ile Trp Asn Ser Ile Tyr Phe Thr Val
260 265 270

Leu Gly Phe Leu Arg Phe Glu Ser Pro Ile Ser Ile Phe Lys Glu Leu
275 280 285

Lys Ala Thr Phe Leu Pro Met Leu Thr Val Gly Ser Phe Gly His Leu
290 295 300

Leu Ile
305

<210> 87

<211> 178

<212> PRT

<213> Arabidopsis thaliana

<400> 87

Met Gln Tyr Tyr Glu Asn Arg Glu Lys Asp Tyr Tyr Glu Val Ala Gln
1 5 10 15

Gly Gln Arg Asn Gly Tyr Gly Gln Ser Gln Ser His Asn His Glu Gly
20 25 30

Tyr Gly Gln Ser Gln Ser Arg Gly Gly Tyr Gly Gln Ile His Asn Arg
35 40 45

Glu Gly Tyr Asn Gln Asn Arg Glu Gly Tyr Ser Gln Ser Gln Ser Arg
50 55 60

Pro Val Tyr Gly Leu Ser Pro Thr Leu Asn His Arg Ser His Gly Gly
65 70 75 80

Phe Leu Asp Gly Leu Phe Lys Gly Gln Asn Gly Gln Lys Gly Gln Ser
85 90 95

Gly Leu Gly Thr Phe Leu Gly Gln His Lys Ser Gln Glu Ala Lys Lys
100 105 110

Ser Gln Gly His Gly Lys Leu Leu Gly Gln His Asp Gln Lys Lys Thr
115 120 125

His Glu Thr Asn Ser Gly Leu Asn Gly Leu Gly Met Phe Ile Asn Asn
130 135 140

Gly Glu Lys Lys His Arg Arg Lys Ser Glu His Lys Lys Lys Asn Lys
145 150 155 160

Asp Gly His Gly Ser Gly Asn Glu Ser Gly Ser Ser Ser Gly Ser Asp
165 170 175

Ser Asp

<210> 88

<211> 202

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<212> PRT

<213> Arabidopsis thaliana

<400> 88

```
Met Gly Cys Val Arg Cys Lys Ser Ser Asp Pro Trp Gln Thr Ser Ala
1               5                  10                  15

Asn Ala Phe Glu Ser Val Asp Glu Ser Gly Ile Asn Glu Ala Trp Val
            20                  25                  30

Glu Ile Ser Ser Arg Arg Ser Phe Val Ala Gly Glu Gly Ser Arg Lys
        35                  40                  45

Lys Leu Glu Arg Lys Lys Ser Gln Val Leu Leu Glu Gly Tyr Val Glu
    50                  55                  60

Thr Ala Ser Ser Ser Ser Val Asp Asp Gln Lys Asp Asp Leu Thr Arg
65                  70                  75                  80

Ser Lys Ser Leu Thr Asp Asp Asp Leu Glu Asp Leu Arg Gly Cys Leu
                85                  90                  95

Asp Leu Gly Phe Gly Phe Ser Tyr Asp Glu Ile Pro Glu Leu Cys Asn
            100                 105                 110

Thr Leu Pro Ala Leu Glu Leu Cys Tyr Ser Met Ser Gln Lys Phe Leu
        115                 120                 125

Asp Asp Lys Gln Asn Lys Ser Pro Glu Thr Ser Ser Val Glu Asp Cys
    130                 135                 140

Pro Ser Pro Pro Leu Val Thr Ala Thr Pro Ile Ala Asn Trp Lys Ile
145                 150                 155                 160

Ser Ser Pro Gly Asp Asn Pro Asp Asp Val Lys Ala Arg Leu Lys Tyr
                165                 170                 175

Trp Ala Gln Ala Val Ala Leu Leu Arg Asp Phe Val Phe Met Arg Ala
            180                 185                 190

Ile Thr Asn Trp Leu Trp Thr Ser Thr Cys
        195                 200
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<210> 89

<211> 638

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<212> PRT

<213> Arabidopsis thaliana

<400> 89

Met Ala Val Asp Ser Arg Met Asp Leu Leu Ser Glu Arg Ala Val Leu
1 5 10 15

Met Arg Ala Ser Leu Gln Lys Ser Gln Thr Ile Thr Asp Asn Val Val
20 25 30

Ser Ile Leu Gly Ser Phe Asp Ser Arg Leu Ser Ala Leu Glu Thr Ala
35 40 45

Met Arg Pro Thr Gln Ile Arg Thr His Ala Ile Arg Lys Ala His Glu
50 55 60

Asn Ile Asp Arg Thr Leu Lys Ala Ala Glu Val Ile Leu Ser Gln Phe
65 70 75 80

Asp Leu Leu Arg Gln Ala Glu Thr Lys Val Leu Lys Gly Pro His Glu
85 90 95

Asp Leu Glu Ser Tyr Leu Asp Ala Ile Ala Gln Leu Arg Lys Ile Ile
100 105 110

Arg Tyr Phe Met Ser Asn Lys Ser Phe Lys Ser Ser Asp Gly Val Leu
115 120 125

Asn His Ala Asn Ser Leu Leu Ala Lys Ala Gln Ser Lys Leu Glu Glu
130 135 140

Glu Phe Lys Gln Leu Leu Ala Ser Tyr Ser Lys Ala Val Glu Pro Asp
145 150 155 160

Arg Leu Phe Asp Gly Leu Pro Asn Ser Leu Arg Pro Ser Ser Asp Gly
165 170 175

Asp Gly Gly Gly Lys Pro His Gly Gly His His Asn Asp Asp Ala Glu
180 185 190

Thr Ala Ala Tyr Thr Leu Pro Ile Leu Ile Pro Ser Arg Val Leu Pro
195 200 205

Leu Leu His Asp Leu Ala Gln Gln Met Val Gln Ala Gly His Gln Gln
210 215 220

```
Gln Leu Leu Gln Ile Tyr Arg Asp Thr Arg Ser Phe Val Leu Glu Glu
225                 230                 235                 240

Ser Leu Lys Lys Leu Gly Val Glu Lys Leu Ser Lys Glu Asp Val Gln
                245                 250                 255

Arg Met Gln Trp Glu Val Leu Glu Ala Lys Ile Gly Asn Trp Ile His
            260                 265                 270

Phe Met Arg Ile Ala Val Lys Leu Leu Phe Ala Gly Glu Arg Gln Val
        275                 280                 285

Cys Asp Gln Ile Phe Arg Gly Phe Asp Ser Leu Ser Asp Gln Cys Phe
    290                 295                 300

Ala Glu Val Thr Val Ser Ser Val Ser Met Leu Leu Ser Phe Gly Asp
305                 310                 315                 320

Ala Ile Ala Arg Ser Lys Arg Ser Pro Glu Lys Leu Phe Val Leu Leu
                325                 330                 335

Asp Met Tyr Glu Ile Met Arg Glu Leu His Thr Glu Ile Glu Thr Ile
            340                 345                 350

Phe Lys Gly Lys Ala Cys Leu Glu Ile Arg Asp Ser Ala Thr Gly Leu
        355                 360                 365

Thr Lys Arg Leu Ala Gln Thr Ala Gln Glu Thr Phe Gly Asp Phe Glu
    370                 375                 380

Glu Ala Val Glu Lys Asp Ala Thr Lys Thr Ala Val Leu Asp Gly Thr
385                 390                 395                 400

Val His Pro Leu Thr Ser Tyr Val Ile Asn Tyr Val Lys Phe Leu Phe
                405                 410                 415

Asp Tyr Gln Thr Thr Leu Lys Gln Leu Phe Leu Glu Phe Gly Asn Gly
            420                 425                 430

Asp Asp Ser Asn Ser Gln Leu Ala Ser Val Thr Met Arg Ile Met Gln
        435                 440                 445

Ala Leu Gln Asn Asn Leu Asp Gly Lys Ser Lys Gln Tyr Lys Asp Pro
    450                 455                 460

Ala Leu Thr His Leu Phe Leu Met Asn Asn Ile His Tyr Met Val Arg
465                 470                 475                 480
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Ser Val Arg Arg Ser Glu Ala Lys Asp Leu Leu Gly Asp Asp Trp Val
485 490 495

Gln Arg His Arg Arg Ile Val Gln Gln His Ala Asn Gln Tyr Lys Arg
500 505 510

Val Ala Trp Thr Lys Ile Leu Gln Ser Ser Ser Ala Gln Gly Leu Thr
515 520 525

Ser Ser Gly Gly Gly Ser Leu Glu Gly Gly Asn Ser Ser Gly Val Ser
530 535 540

Arg Gly Leu Leu Lys Glu Arg Phe Lys Met Phe Asn Met Gln Phe Asp
545 550 555 560

Glu Leu His Gln Arg Gln Ser Gln Trp Thr Val Pro Asp Thr Glu Leu
565 570 575

Arg Glu Ser Leu Arg Leu Ala Val Ala Glu Val Leu Leu Pro Ala Tyr
580 585 590

Arg Ser Phe Leu Lys Arg Phe Gly Pro Leu Val Glu Ser Gly Lys Asn
595 600 605

Pro Gln Lys Tyr Ile Lys Tyr Thr Ala Glu Asp Leu Glu Arg Leu Leu
610 615 620

Gly Glu Leu Phe Glu Gly Lys Ser Met Asn Gln Pro Arg Arg
625 630 635

<210> 90

<211> 526

<212> PRT

<213> Arabidopsis thaliana

<400> 90

Met Asp Pro Trp Ser Trp Ile Cys Glu Leu Pro Glu Asp Pro Glu Phe
1 5 10 15

Ser Glu Ser Asp Ser His Ala Val Phe Gln Leu Ala Gly Asp Leu Thr
20 25 30

Arg Ser Ile Lys Leu Arg Ala Glu Arg Thr Leu Gly Ser Asp Gln Glu
35 40 45

Ser His Ser Leu Thr Phe Thr Val Val Ala Glu Gly Phe Asn Leu Leu
50 55 60

Lys Ser Ser Thr Ile Trp Val Ser Asn Thr Cys Pro Leu Ser Ser Glu
65 70 75 80

Lys Pro Phe Leu Pro Leu Val Leu Gln Leu Leu Gln Glu Leu Ile Thr
85 90 95

Arg Ser Pro Thr Thr His Asp Gly Ala Cys Thr Lys Phe Glu Gln Leu
100 105 110

Glu Ile Lys Pro Ser Pro Val Ser Trp Val Met Asp Ser His Ser Pro
115 120 125

Glu Ser Phe Ser Ser Val Phe Asn Leu Ile Leu Leu Thr Arg Leu Phe
130 135 140

Trp Leu Cys Val Phe Asp Ala Pro Ser Glu Val Gly Ser Phe Phe Phe
145 150 155 160

Gln His Leu Leu Gly Pro His Val Asn Ala Leu Thr Cys Gln His Ala
165 170 175

Pro Val Leu Arg Thr Phe Leu Val Ser Leu Gly Val Asp Ala Glu Leu
180 185 190

Cys Ile Val Arg Ala Ala Ser Tyr Ala Leu Ser Lys Trp Met Ile Ser
195 200 205

Lys Glu Ile Gly Leu Gly Asn Leu Gly Leu Lys Gln Phe Ser Ser Ser
210 215 220

Leu Met Pro Arg His Ser Leu Gly Phe Ser Tyr Ala Thr Glu Ala His
225 230 235 240

Gly Leu Trp Ile Leu Lys Gly Tyr Phe Pro Ile Leu Ser Met Asn Val
245 250 255

Thr Asn Asn Ser Ser Asn Glu Val His Asn Lys Ile Val Lys Phe Pro
260 265 270

Phe Val Glu Pro Lys Glu Ala Val Leu Arg Tyr Ala Leu Ser His Gln
275 280 285

Gln Ala Glu Ile Leu Val Gln Phe Glu Tyr Ser Val Lys Phe Tyr Glu
290 295 300

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Asn Tyr Ile Lys Val Asn Ala Arg Val Asp Asn Ile Arg Ile His Val
305 310 315 320

Ser Lys Leu Gly Phe His Lys Gly Gly Val Gly Val Glu Asn Gln Ile
325 330 335

Ala Asp Cys Tyr Ser Glu Glu Arg Tyr Phe Pro Ser Arg Val Arg Val
340 345 350

Trp Leu Gly Pro Glu Leu Gly Ser Ser His Val Ser Gly Leu Ser Leu
355 360 365

Gly Arg Ser Thr Lys Asn Glu Glu Arg Asp Ile Glu Val Thr Arg Val
370 375 380

Leu Lys Gly Asn Phe Gly Lys Gly Lys Val Ala Pro Arg Val Lys Ala
385 390 395 400

Arg Ala Arg Met Ala Thr Lys Arg Lys Val Lys Asp Trp Arg Ile Glu
405 410 415

Gln Glu Ser Glu Gly Asn Ala Ala Val Phe Asp Ala Val Leu Tyr Asp
420 425 430

Arg Glu Ser Gly Gln Glu Val Thr Thr Val Lys Pro Lys Pro Asn Gln
435 440 445

Glu Gly Leu Lys Asn Val Phe Thr Lys Ser Gly Gly Met Val Phe Gly
450 455 460

Arg Asp Glu Tyr Gly Asp Glu Val Gly Trp Arg Val Gly Arg Glu Met
465 470 475 480

Glu Gly Ser Val Leu Lys Trp Arg Leu Gly Gly Lys Ile Trp Leu Thr
485 490 495

Tyr Trp Pro Asn Lys Leu Asn Thr Leu Phe Tyr Glu Thr Arg Cys Val
500 505 510

Glu Trp Cys Asp Glu Val Asp Leu Pro Leu Leu Pro Thr Ser
515 520 525

<210> 91

<211> 306

<212> PRT

<213> Arabidopsis thaliana

<400> 91

Met Glu Val Pro Val Ile Asn Arg Ile Arg Asp Phe Glu Val Gly Ile
1 5 10 15

Asn Ser Ile Asn Asp Pro Ser Phe Leu Ser Arg Ser Val Ala Val Ser
20 25 30

Gly Ile Gly Lys Leu His Gln Ala Tyr Gly Phe Trp Lys Trp Gly Ala
35 40 45

Leu Ile Ile Ala Phe Leu Ala Tyr Phe Thr Asn Phe Val Ser Lys Leu
50 55 60

Asn Ser Leu Val Val Arg Leu Arg Lys Ile Asp Val Ser Val Ser Ser
65 70 75 80

Pro Thr Leu Phe Asp Asp Tyr Asp Ser Asp Ser Asp Val Ser Cys Ser
85 90 95

Ser Thr Val Ser Ser Asp Asp Glu Lys Asp Glu Glu Asp Glu Ala Asp
100 105 110

Asp Glu Asp Glu Asp Val Asp Ser Ile Phe Asn Arg Arg Arg Val Asn
115 120 125

Gly Gly Phe Arg Val Arg Gly Ser Asp Tyr Tyr Asp Asp Asp Asp Asp
130 135 140

Gln Gly Asp Asn Gly Asn Cys Thr Trp Met Gly Arg Arg Tyr Ser Gly
145 150 155 160

Ser Phe Gly Asp Leu Phe Ser Trp Pro Asp Leu Gly Gly Ile Gly Ser
165 170 175

Ser Gly Val Val Lys Leu Trp Asp His Leu Asp Ile Asp Gly Asp Asp
180 185 190

His Glu Asn Val Val Ala Thr Phe Leu Lys Asn Tyr Asn Ser Thr Ser
195 200 205

Ser Pro Phe Phe Trp Ala Ala Glu Lys Lys Gly Val Asp Ala Val Lys
210 215 220

Val Lys Ala Cys Asp Pro Arg Ala Gly Phe Arg Met Pro Ala Leu Leu
225 230 235 240

Ala Glu Trp Arg Gln Pro Gly Arg Leu Leu Gly Asn Ile Ile Gly Val
245 250 255

Asp Thr Gly Gly Val Glu Lys Val Tyr Val Arg Asp Asp Val Ser Gly
260 265 270

Glu Ile Ala Val Gly Asp Leu Arg Lys Phe Asn Gly Val Leu Thr Asp
275 280 285

Leu Thr Glu Cys Glu Ala Glu Thr Trp Trp Asp Ala Asp Val Leu Ile
290 295 300

Ser Gly
305

<210> 92

<211> 332

<212> PRT

<213> Arabidopsis thaliana

<400> 92

Met Ile Ala Leu Ala Ala Ser Ser Leu Gly Asn Thr Pro Ile Ala Ser
1 5 10 15

Phe Asn Arg His Phe Arg Phe Arg Leu His Pro Arg Asn Pro Leu Ile
20 25 30

Gln Ala Ala Val Ser Pro Ser Ser Ser Ser Ser Ser Pro Thr Ala Ser
35 40 45

Ser Gly Phe Asp Leu Ser Ser Leu Glu Ser Ala Ile Asn Lys Lys Asp
50 55 60

Ser Asn Gly Val Lys Glu Ala Leu Asp Lys Leu Ser Glu Glu Gly Trp
65 70 75 80

Ala Lys Lys Trp Ser Ser Gln Pro Tyr Leu Ser Arg Arg Thr Thr Ser
85 90 95

Leu Arg Glu Leu Thr Thr Leu Gly Ile Lys Asn Ala Glu Thr Leu Ala
100 105 110

Ile Pro Ser Val Arg Asn Asp Ala Ala Phe Leu Phe Thr Val Val Gly
115 120 125

Ser Thr Gly Phe Ile Ala Val Leu Ala Gly Gln Leu Pro Gly Asp Trp
130 135 140

Gly Phe Phe Val Pro Tyr Leu Val Gly Ser Ile Ser Leu Val Val Leu
145 150 155 160

Ala Val Gly Ser Val Ser Pro Gly Leu Leu Gln Ala Ala Ile Ser Gly
165 170 175

Phe Ser Thr Phe Phe Pro Asp Tyr Gln Glu Arg Ile Ala Ala His Glu
180 185 190

Ala Ala His Phe Leu Val Ala Tyr Leu Ile Gly Leu Pro Ile Leu Gly
195 200 205

Tyr Ser Leu Asp Ile Gly Lys Glu His Val Asn Leu Ile Asp Glu Arg
210 215 220

Leu Ala Lys Leu Ile Tyr Ser Gly Lys Leu Asp Ser Lys Glu Leu Asp
225 230 235 240

Arg Leu Ala Ala Val Ala Met Ala Gly Leu Ala Ala Glu Gly Leu Lys
245 250 255

Tyr Asp Lys Val Ile Gly Gln Ser Ala Asp Leu Phe Ser Leu Gln Arg
260 265 270

Phe Ile Asn Arg Ser Gln Pro Lys Ile Ser Asn Glu Gln Gln Gln Asn
275 280 285

Leu Thr Arg Trp Ala Val Leu Tyr Ser Ala Ser Leu Leu Lys Asn Asn
290 295 300

Lys Thr Ile His Glu Ala Leu Met Ala Ala Met Ser Lys Asn Ala Ser
305 310 315 320

Val Leu Glu Cys Ile Gln Thr Ile Glu Thr Ala Ser
325 330

<210> 93

<211> 130

<212> PRT

<213> Arabidopsis thaliana

<400> 93

Met Ala Ser Pro Lys Ser Pro Thr Arg Pro Thr Gln Gln Asn Pro Gln
1 5 10 15

Pro Asn Phe His Asp Phe Leu Pro Thr Met Ala Gly Asn Leu Gly Gly
20 25 30

Glu Gly Leu Ile Gly Glu Leu Cys Asn Gly Phe Glu Leu Leu Met Asp
35 40 45

Arg Glu Lys Gly Val Ile Thr Phe Glu Ser Leu Arg Arg Asn Ala Ala
50 55 60

Ala Val Leu Gly Leu Gly Asp Leu Thr Asp Glu Asp Val Arg Cys Met
65 70 75 80

Ile Lys Glu Gly Asp Phe Asp Cys Asp Gly Ala Leu Asn Gln Met Glu
85 90 95

Phe Cys Val Leu Met Phe Arg Leu Ser Pro Asp Leu Met Glu Ala Ser
100 105 110

Arg Cys Leu Val Thr Glu Val Ile Glu Glu Glu Phe Gly Phe Thr Arg
115 120 125

Arg His
130

<210> 94

<211> 1088

<212> PRT

<213> Arabidopsis thaliana

<400> 94

Met Gly Leu Leu Lys Thr Ser Trp Leu Leu Leu Leu Phe Trp Val Val
1 5 10 15

Ser Ser Pro Leu Cys Phe Arg Phe His Tyr Cys Tyr Gly Ser Glu Leu
20 25 30

Ser Val Lys Phe Leu Lys Ala Pro Pro Thr Thr Ser Arg Phe Thr Ser
35 40 45

Ala Lys Phe Ser Phe Leu Ala Phe Glu Asp Gly Asn Arg Thr Cys Ser
50 55 60

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Ser Cys Lys Phe Arg Cys Lys Leu Asp Asp Arg Ile Ser Leu Asp Cys
65                  70                  75                  80

His Gln Arg Lys Val Ser Tyr Ser Lys Leu Leu Asp Gly Asp His Thr
                85                  90                  95

Leu Glu Val Cys Ala Asn Arg Met His Gly Phe Gly Cys Asn His Tyr
            100                 105                 110

Asn Trp Thr Val Asp Thr Val Ser Pro Thr Ala Phe Val Thr Ala Ser
        115                 120                 125

Met Pro Phe Thr Ser Ala Gln Asn Val Ser Val Asn Ile Thr Phe Thr
    130                 135                 140

Glu Pro Cys Val Gly Arg Gly Gly Phe Gly Cys Ser Ser Val Asn Ser
145                 150                 155                 160

Cys Asp Leu Leu Val Tyr Gly Ala Gly Gln Val Ile Pro Ser Ser Phe
                165                 170                 175

Thr Val Leu Asp Gln Tyr Leu Arg Tyr Ser Leu Leu Val Gly Leu Ser
            180                 185                 190

Pro Asp Ala Gln Tyr Gly Arg Ile Val Leu Val Met Asn Lys Ser Val
        195                 200                 205

Cys Ser Asp Ile Ala Gly Asn Asn Phe Lys Arg Ala Leu Gly Ser Arg
    210                 215                 220

Phe Phe Val His Phe Asp Arg Arg Asn Val Leu Val Asn Leu Arg Thr
225                 230                 235                 240

His Val Pro Glu Lys Leu Leu Lys Leu Asn Asn Gln Thr Arg Thr Val
                245                 250                 255

Gln Ala Thr Asn Asp Asn Asn Lys Leu Asn Val Tyr Leu Tyr Phe Ser
            260                 265                 270

Glu Pro Val Leu Asn Ser Ser Ala Glu Ile Leu Arg Arg Leu Asn Thr
        275                 280                 285

Asn Gln Gly Asp Leu Leu Pro Ile Asp Gly Asn Thr Asn Gly Asn Arg
    290                 295                 300

Arg Phe Ala Phe Met Val Thr Asn Thr Ser Arg Arg Ala Ile Val Thr
305                 310                 315                 320
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Val Thr Leu Asp Ser Asn Ser Ile Arg Ser Arg His Gly Thr Pro Ala
                325                 330                 335

Ser Pro Thr Ala Pro Leu Thr Phe Leu Tyr Asp Thr Glu Arg Pro His
            340                 345                 350

Val Ile Leu Asn Thr Thr Ser Gly Met Arg Thr Arg Lys His Thr Ile
        355                 360                 365

Pro Val Trp Ile Lys Phe Met Lys Pro Val Phe Gly Phe Asn Ser Ser
    370                 375                 380

Phe Val Ser Ile Ser Gly Gly Tyr Leu Asp Ser Phe Glu Glu Leu Ser
385                 390                 395                 400

Gly Ser Ile Tyr Ile Val Tyr Val Lys Ala Asn Thr Ser Thr Leu Ser
                405                 410                 415

Ile Lys Ile Pro Glu Asn Val Thr Gln Asp Val Ala Gly Asn Lys Asn
            420                 425                 430

Leu Ala Ser Asn Ile Leu Lys Val Lys His Tyr Ser Val Pro Met Ile
        435                 440                 445

Ser Ser Val Ile Ser Trp Val Thr Thr Tyr Ile Phe Leu Val Thr Ser
    450                 455                 460

Phe Val Ala Gly Leu Leu Thr Leu Ser Thr Thr Ser Leu Tyr Ser Leu
465                 470                 475                 480

Gly Ala Phe Pro Arg Pro Ser Pro Tyr Leu Ile Ser Asp Pro Thr Arg
                485                 490                 495

Asn Leu Phe Arg Thr Ala Cys His Ile Gln Phe Phe Ala Leu Thr Arg
            500                 505                 510

Trp Leu Pro Val Thr Leu Pro Val Asp Tyr Tyr Glu Leu Val Arg Gly
        515                 520                 525

Ile Gln Trp Ile Ile Pro Tyr Phe Pro Leu Pro Trp Glu Thr Lys Ile
    530                 535                 540

Lys Glu Gln Ile Met Val Ala Thr Ser Pro Tyr Ile Gly Pro His Ser
545                 550                 555                 560

Phe Ile Ser Lys Thr His Asn Asn Met Ile Asn Leu Lys Thr Ser Thr
                565                 570                 575
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Asn Ala Glu Ser Val Phe Gly Leu Pro Leu Thr Ala Met Glu Tyr Arg
580 585 590

Leu Phe Phe Glu Thr Ser Asn Leu Lys Pro Glu Ala Glu His Val Leu
595 600 605

Gly Leu Pro His Ser Thr Val Trp Arg Asp Phe Asn Arg Ile Met Phe
610 615 620

Trp Ile Ala Ile Ile Gly Gly Ser Leu Val Leu Leu His Ile Val Leu
625 630 635 640

Ser Leu Ile Leu Lys Phe Lys Lys Ala His Ser Glu Lys Lys Arg Ser
645 650 655

Phe Gly Ala Phe Val Phe Pro Arg Phe Glu Leu Phe Leu Leu Ile Leu
660 665 670

Ala Leu Pro Ser Ile Cys Lys Ala Ala Arg Ser Leu Ile Gln Gly Tyr
675 680 685

Phe Lys His Gln Gly Ala Ala Glu Ala Ser Val Ile Val Gly Ile Leu
690 695 700

Val Leu Cys Val Val Ala Ile Leu Leu Leu Ala Leu Phe Leu Phe Leu
705 710 715 720

Ser Val Gly Ile Thr Phe Gly Lys Leu Leu Gln Tyr Lys Glu Ile His
725 730 735

Gln Glu Gly Gln Thr Phe His Trp Tyr Gln Glu Leu Ile Arg Val Thr
740 745 750

Leu Gly Pro Gly Lys Arg Gly Gln Trp Thr Trp Lys Thr Glu Asn Ser
755 760 765

Val Tyr Leu Thr Arg Leu Gly Pro Val Phe Glu Asp Leu Arg Gly Pro
770 775 780

Pro Lys Tyr Met Leu Thr Gln Ile Ser Gly Ser Asn Pro Leu Lys Gln
785 790 795 800

Gln Asp Asp Arg Ile Ile Ala Ser Asp Asp Gln Asn Glu Asp Ala Glu
805 810 815

Ala Pro Cys Ile Gln Lys Leu Phe Gly Ile Leu Arg Ile Tyr Tyr Thr
820 825 830

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```
Phe Leu Glu Thr Val Lys Arg Val Cys Leu Gly Ile Ile Ala Gly Ala
        835                 840                 845

Phe Leu Asp Asn Glu Thr Ala Lys Thr Pro Ile Val Val Leu Leu Ser
    850                 855                 860

Ile Thr Ser Phe Gln Leu Phe Phe Leu Leu Leu Lys Lys Pro Phe Ile
865                 870                 875                 880

Lys Lys Lys Val Gln Leu Val Glu Ile Ile Ser Ile Ala Cys Gln Val
                885                 890                 895

Gly Val Phe Ala Ser Cys Leu Met Leu Leu Ala Lys Asp Phe Pro Glu
            900                 905                 910

Ala Ser Gly Lys Lys Leu Gly Ile Phe Met Val Val Leu Phe Leu Ile
        915                 920                 925

Gly Phe Ile Met Leu Met Cys Asn Glu Trp Tyr Ser Leu Tyr Lys Gln
    930                 935                 940

Thr Lys Arg Leu Asp Gln Ile Asn Arg Ser Phe Leu Ser Gly Leu Lys
945                 950                 955                 960

Met Phe Ile Ile Gly Leu Ala Ala Leu Ile Leu Pro Gln Lys Met Ile
                965                 970                 975

Lys Asn Lys Ile Pro Val Ala Gln Leu Glu Ala Arg Ser Ser Ser Asn
            980                 985                 990

Gly Gly Thr Thr Pro Glu Phe Arg Tyr Arg Asn Ser Ser Gly Ser Arg
        995                 1000                1005

Ser Ser Gly Ser Leu Asp Lys Pro Trp Leu Lys Gln Ile Arg Glu
    1010                1015                1020

Met Ala Lys Ser Ser Phe Thr Arg Asp Arg Ser Asn Ser Lys Val
    1025                1030                1035

Pro Ser Asp Pro Ser Cys Ser Lys Ser Gly Trp Ser Ser Ser Ile
    1040                1045                1050

Trp Gly Thr Lys Thr Ser Gly Ser Ser Ser Lys Glu Ser Ser Ala
    1055                1060                1065

Asp Tyr Lys Ser Arg Pro Lys Gly Leu Tyr Lys Asp Leu Glu Ala
    1070                1075                1080
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Ile Phe Ala Ser Lys
1085

<210> 95

<211> 271

<212> PRT

<213> Arabidopsis thaliana

<400> 95

Met Gly Leu Leu Ser Leu Glu Asp Thr Ile Lys Glu Lys Leu Lys Asp
1 5 10 15

Arg Lys Asn Ala His Phe Met Leu Val Asp Gly Met Ser Lys Leu Leu
20 25 30

Thr Glu Lys Val Lys Asn Cys Gln Ser Leu Asp Phe Gln Val Ser Gly
35 40 45

Val Lys Trp Arg Leu Val Ile Arg Leu Ser Arg Gly Arg Lys Asp His
50 55 60

Leu Ser Phe Val Leu Glu Ile Thr Asp Glu Lys Cys Thr Gly Ser Thr
65 70 75 80

Trp Asp Val Lys Phe Asn Phe Lys Ile Gly Ile Val Pro Gln Thr Gly
85 90 95

Pro Asp Tyr Cys Phe Val Leu Val Gly His Gln Asn Glu Lys Lys Arg
100 105 110

Ser Gln Gly Leu Ala Asn Phe Ile Ser His Thr Asp Leu Lys Glu Arg
115 120 125

Phe Leu Val Asn Asp Lys Ala Gly Phe Tyr Ala Glu Ile Ser Asp Val
130 135 140

Gln Pro Asn Phe Pro Val Thr Arg Ile Pro Arg Thr Met Gly Thr Ala
145 150 155 160

Glu Arg Phe Lys Leu Ile Glu Phe Ser Pro Lys Asn Ser Arg Phe Thr
165 170 175

Trp Lys Ile Thr Gln Phe Ser Ser Phe Asp Gly Glu Glu His Ser Ser
180 185 190

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Tyr Glu Phe Thr Val Gly Pro Arg Arg Trp Lys Leu Val Met Tyr Pro
195 200 205

Lys Gly Asn Gly Asp Gly Lys Gly Asn Ser Leu Ser Leu Tyr Leu Phe
210 215 220

Ala Ser Asp Tyr Val Thr Asn Gly Pro Lys Gly Gly Thr Leu Ala Ile
225 230 235 240

Tyr Lys Leu Arg Val Leu Asp Gln Leu Asn Arg Asn His Cys Glu Thr
245 250 255

Gly Met Cys Ile Tyr Thr Leu Asn Ser Leu Ile Tyr Thr Phe Phe
260 265 270

<210> 96

<211> 137

<212> PRT

<213> Arabidopsis thaliana

<400> 96

Met Glu Asp Val Lys Gly Lys Glu Ile Ile Asp Asp Ala Pro Ile Asp
1 5 10 15

Asn Lys Val Ser Asp Glu Met Glu Ser Glu Glu Asn Ala Ile Lys Lys
20 25 30

Lys Tyr Gly Gly Leu Leu Pro Lys Lys Ile Pro Leu Ile Ser Lys Asp
35 40 45

His Glu Arg Ala Phe Phe Asp Ser Ala Asp Trp Ala Leu Gly Lys Gln
50 55 60

Lys Gly Gln Lys Pro Lys Gly Pro Leu Glu Ala Leu Arg Pro Lys Leu
65 70 75 80

Gln Pro Thr Pro Gln Gln Gln Pro Arg Ala Arg Arg Met Ala Tyr Ser
85 90 95

Ser Gly Glu Thr Glu Asp Thr Glu Ile Asp Asn Asn Glu Ala Pro Asp
100 105 110

Asp Gln Ala Cys Ala Ser Ala Val Asp Ser Thr Asn Leu Lys Asp Asp
115 120 125

Gly Gly Ala Lys Asp Asn Ile Lys Ser
130 135

<210> 97

<211> 340

<212> PRT

<213> Arabidopsis thaliana

<400> 97

Met Met Phe Ser Val Thr Val Ala Ile Leu Val Cys Leu Ile Gly Tyr
1 5 10 15

Ile Tyr Arg Ser Phe Lys Pro Pro Pro Pro Arg Ile Cys Gly His Pro
20 25 30

Asn Gly Pro Pro Val Thr Ser Pro Arg Ile Lys Leu Ser Asp Gly Arg
35 40 45

Tyr Leu Ala Tyr Arg Glu Ser Gly Val Asp Arg Asp Asn Ala Asn Tyr
50 55 60

Lys Ile Ile Val Val His Gly Phe Asn Ser Ser Lys Asp Thr Glu Phe
65 70 75 80

Pro Ile Pro Lys Asp Val Ile Glu Glu Leu Gly Ile Tyr Phe Val Phe
85 90 95

Tyr Asp Arg Ala Gly Tyr Gly Glu Ser Asp Pro His Pro Ser Arg Thr
100 105 110

Val Lys Ser Glu Ala Tyr Asp Ile Gln Glu Leu Ala Asp Lys Leu Lys
115 120 125

Ile Gly Pro Lys Phe Tyr Val Leu Gly Ile Ser Leu Gly Ala Tyr Ser
130 135 140

Val Tyr Ser Cys Leu Lys Tyr Ile Pro His Arg Leu Ala Gly Ala Val
145 150 155 160

Leu Met Val Pro Phe Val Asn Tyr Trp Trp Thr Lys Val Pro Gln Glu
165 170 175

Lys Leu Ser Lys Ala Leu Glu Leu Met Pro Lys Lys Asp Gln Trp Thr
180 185 190

Phe Lys Val Ala His Tyr Val Pro Trp Leu Leu Tyr Trp Trp Leu Thr
195 200 205

Gln Lys Leu Phe Pro Ser Ser Ser Met Val Thr Gly Asn Asn Ala Leu
210 215 220

Cys Ser Asp Lys Asp Leu Val Val Ile Lys Lys Lys Met Glu Asn Pro
225 230 235 240

Arg Pro Gly Leu Glu Lys Val Arg Gln Gln Gly Asp His Glu Cys Leu
245 250 255

His Arg Asp Met Ile Ala Gly Phe Ala Thr Trp Glu Phe Asp Pro Thr
260 265 270

Glu Leu Glu Asn Pro Phe Ala Glu Gly Glu Gly Ser Val His Val Trp
275 280 285

Gln Gly Met Glu Asp Arg Ile Ile Pro Tyr Glu Ile Asn Arg Tyr Ile
290 295 300

Ser Glu Lys Leu Pro Trp Ile Lys Tyr His Glu Val Leu Gly Tyr Gly
305 310 315 320

His Leu Leu Asn Ala Glu Glu Glu Lys Cys Lys Asp Ile Ile Lys Ala
325 330 335

Leu Leu Val Asn
340

<210> 98

<211> 326

<212> PRT

<213> Arabidopsis thaliana

<400> 98

Met Thr Asn Gly Gly Arg Gly Ser Gly Gly Gly Gly Gly Gly Gly Gly
1 5 10 15

Arg Glu Ser Gly Gly Arg Asp Leu Glu Ile Arg Pro Gly Gly Met Leu
20 25 30

Val Gln Lys Arg Asn Pro Asp Leu Asp Pro Val Gly Pro Pro Pro Pro
35 40 45

Pro Met Ile Arg Val Arg Ile Lys Tyr Gly Ala Val Tyr His Glu Ile
50 55 60

Asn Ile Ser Pro Gln Ala Ser Phe Gly Glu Leu Lys Lys Met Leu Thr
65 70 75 80

Gly Pro Thr Gly Ile His His Gln Asp Gln Lys Leu Met Tyr Lys Asp
85 90 95

Lys Glu Arg Asp Ser Lys Ala Phe Leu Asp Val Ser Gly Val Lys Asp
100 105 110

Lys Ser Lys Met Val Leu Ile Glu Asp Pro Leu Ser Gln Glu Lys Arg
115 120 125

Phe Leu Glu Met Arg Lys Ile Ala Lys Thr Glu Lys Ala Ser Lys Ala
130 135 140

Ile Ser Asp Ile Ser Leu Glu Val Asp Arg Leu Gly Gly Arg Val Ser
145 150 155 160

Ala Phe Glu Met Val Thr Lys Lys Gly Gly Lys Ile Ala Glu Lys Asp
165 170 175

Leu Val Thr Val Ile Glu Leu Leu Met Asn Glu Leu Ile Lys Leu Asp
180 185 190

Ala Ile Val Ala Glu Gly Asp Val Lys Leu Gln Arg Lys Met Gln Val
195 200 205

Lys Arg Val Gln Asn Tyr Val Glu Thr Leu Asp Ala Leu Lys Val Lys
210 215 220

Asn Ser Met Ala Asn Gly Gln Gln Lys Gln Ser Ser Thr Ala Gln Arg
225 230 235 240

Leu Ala Pro Ile Gln Glu His Asn Asn Glu Glu Arg Gln Glu Gln Lys
245 250 255

Pro Ile Gln Ser Leu Met Asp Met Pro Ile Gln Tyr Lys Glu Lys Lys
260 265 270

Gln Glu Ile Glu Glu Glu Pro Arg Asn Ser Gly Glu Gly Pro Phe Val
275 280 285

Leu Asp Ser Ser Ala Lys Trp Glu Thr Phe Asp His His Pro Val Thr
290 295 300

Pro Leu Ser Ser Thr Thr Ala Lys Asn Asn Ala Ile Pro Pro Arg Phe
305 310 315 320

Asn Trp Glu Phe Phe Asp
325

<210> 99

<211> 189

<212> PRT

<213> Arabidopsis thaliana

<400> 99

Met Ala Lys Ser Pro Val Glu Val Asn Leu Ile Pro Ile Glu Ala Thr
1 5 10 15

Pro Glu Asn Phe Ala Glu Tyr Gly Gln Val Ile Glu Ala Ser Arg Asp
20 25 30

Gly Ala Gly Phe Gly Pro His Asp Ala Gln Leu Asp Leu Ser Arg Gly
35 40 45

Thr Pro Arg Leu Tyr Ile Leu Arg Leu Lys Glu Thr Pro Leu Gly Phe
50 55 60

Phe Lys Ile Thr His His Ala Lys Val Thr Gln Cys Leu Gly Ser Ile
65 70 75 80

Gly Gly Asp Val Trp Tyr Met Gly Val Ala Lys Pro Ser Leu Ile Glu
85 90 95

Asp Asp Asp Asp Asp Gly Arg Ser Val Asp Thr Val Lys Ser Lys Ser
100 105 110

Gly His Leu Tyr Ile Pro Pro Glu Val Glu Glu Ile Arg Val Phe Arg
115 120 125

Phe Ser Gly Pro Lys Phe Val Lys Leu His Arg Gly Thr Trp His Ala
130 135 140

Gly Pro Leu Phe Ser Gly Ser Ser Phe Met Asp Phe Tyr Asn Leu Glu
145 150 155 160

Leu Ser Asn Thr Asn Val Val Asp His Thr Ser His Asp Phe Thr Lys
165 170 175

Asn Asn Gly Val Ser Phe Gly Phe Asp Thr Leu Ser Ser
180 185

<210> 100

<211> 182

<212> PRT

<213> Arabidopsis thaliana

<400> 100

Met Ala Ser Ser Leu Gln Ser Ser Gly Met Leu Thr Lys Glu Gln Met
1 5 10 15

Val Tyr Leu Phe Asp Arg Phe Asp Tyr Leu Thr Ser Gln Ser Asp Val
20 25 30

Lys Lys Arg Ile Ser Asp Ala Val Asp Asp Lys Gln Glu Ala Val Ala
35 40 45

Val Thr Thr Ala Ile Gln Glu Glu Ile Phe Leu Glu Met Gly Ile Asp
50 55 60

Pro Gly Phe Gly Ile Gly Cys Leu Gly Lys Leu Asn Ser Ala Tyr Glu
65 70 75 80

Asn Asp Lys Glu Leu Met Ile Gly Phe Tyr Lys Phe Leu Ala Lys Glu
85 90 95

Glu Met Ala Cys Glu Glu Ala Glu Leu Gly Gln Asp Gly Phe Glu Gln
100 105 110

Lys Met Lys Ala Leu Gln Gln Leu Gln Glu Gln Gln Leu Glu Met Leu
115 120 125

Lys Tyr Met Arg Lys Phe Ser Leu Asp Asp Gln Ser Ala Ile Leu Gln
130 135 140

Lys Leu Gln Lys Gln Leu Glu Asn Ala Gly Phe Glu Pro Glu Ala Ser
145 150 155 160

Leu Leu Ser Gly Glu Glu Met Glu Glu Ala Gly Arg Arg Arg Val Ser
165 170 175

Pro Val Phe Gly Ser Arg
180

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<210> 101

<211> 108

<212> PRT

<213> Arabidopsis thaliana

<400> 101

Met Ala Ile Ile Ala Ser Thr Phe Gly Thr Gly Leu Ser Tyr Ala Gly
1 5 10 15

Glu Leu Pro Phe Lys Pro Val Thr Gly Gly Glu Val Gly Arg Lys Gln
20 25 30

Gln Arg Met Val Val Val Arg Ala Glu Gly Gly Gly Gly Ile Asn Pro
35 40 45

Glu Ile Arg Lys Asn Glu Asp Lys Val Val Asp Ser Val Val Val Thr
50 55 60

Glu Leu Ser Lys Asn Ile Thr Pro Tyr Cys Arg Cys Trp Arg Ser Gly
65 70 75 80

Thr Phe Pro Leu Cys Asp Gly Ser His Val Lys His Asn Lys Ala Asn
85 90 95

Gly Asp Asn Val Gly Pro Leu Leu Leu Lys Lys Gln
100 105

<210> 102

<211> 185

<212> PRT

<213> Arabidopsis thaliana

<400> 102

Met Gly Leu Ile Pro Gln Pro Gln Glu Ser Ile Gln Glu Ser His Tyr
1 5 10 15

Tyr Thr His Lys Leu Phe Leu Thr Ala Asn Tyr Val Leu Leu Gly Ala
20 25 30

Ser Ser Ser Cys Ile Phe Leu Thr Leu Ser Leu Arg Leu Ile Pro Ser
35 40 45

Leu Cys Gly Phe Phe Leu Ile Leu Leu His Ala Thr Thr Ile Ala Ala
50 55 60

Ala Val Ser Gly Cys Ala Ala Ala Ser Tyr Gly Lys Asn Arg Trp Tyr
65 70 75 80

Ala Ala His Met Ile Ala Thr Val Leu Thr Ala Ile Phe Gln Gly Ser
85 90 95

Val Ser Val Leu Ile Phe Thr Asn Thr Ser Asn Phe Leu Glu Ser Leu
100 105 110

Asn Ser Tyr Val Arg Glu Lys Glu Ala Ser Met Ile Leu Lys Leu Ala
115 120 125

Gly Gly Leu Cys Val Val Ile Phe Cys Leu Glu Trp Ile Val Leu Val
130 135 140

Leu Ala Phe Phe Leu Lys Tyr Tyr Ala Tyr Val Asp Gly Asp Asn Asn
145 150 155 160

Gly Val Ala Met Lys Arg Thr Gly Lys Val Gln Ser Glu Glu Thr Leu
165 170 175

Lys Asn Ser Pro Trp Ala Phe Gln Val
180 185

<210> 103

<211> 181

<212> PRT

<213> Arabidopsis thaliana

<400> 103

Met Ala Arg Arg Asp Val Leu Leu Pro Phe Leu Leu Leu Leu Ala Thr
1 5 10 15

Val Ser Ala Val Ala Phe Ala Glu Asp Asp Pro Asp Cys Val Tyr Thr
20 25 30

Phe Tyr Leu Arg Thr Gly Ser Ile Trp Lys Ala Gly Thr Asp Ser Ile
35 40 45

Ile Ser Ala Arg Ile Tyr Asp Lys Asp Gly Asp Tyr Ile Gly Ile Lys
50 55 60

Asn Leu Gln Ala Trp Ala Gly Leu Met Gly Pro Asp Tyr Asn Tyr Phe
65 70 75 80

Glu Arg Gly Asn Leu Asp Ile Phe Ser Gly Arg Ala Pro Cys Leu Pro
85 90 95

Ser Pro Ile Cys Ala Leu Asn Leu Thr Ser Asp Gly Ser Gly Asp His
100 105 110

His Gly Trp Tyr Val Asn Tyr Val Glu Ile Thr Thr Ala Gly Val His
115 120 125

Ala Gln Cys Ser Thr Gln Asp Phe Glu Ile Glu Gln Trp Leu Ala Thr
130 135 140

Asp Thr Ser Pro Tyr Glu Leu Thr Ala Val Arg Asn Asn Cys Pro Val
145 150 155 160

Lys Leu Arg Asp Ser Val Ser Arg Val Gly Ser Glu Ile Arg Lys Lys
165 170 175

Leu Ser Trp Val Val
180

<210> 104

<211> 369

<212> PRT

<213> Arabidopsis thaliana

<400> 104

Met Leu Gly Ala Gly Phe Gln Leu Thr Arg Gly Arg His Gly Asp Asp
1 5 10 15

Pro Phe Tyr Thr Ser Ala Lys Thr Arg Arg Ala Asn Gln Arg Ile Asp
20 25 30

Gln Leu Arg Arg Ala Gln Ser Asp Val Ser Asn Val Pro Ser Ser Ala
35 40 45

Pro Ser Pro His Lys Gln Gln Leu Glu Pro Ser Asp Leu Ser Ser Ser
50 55 60

Asn Leu Asp Arg Phe Leu Glu Ser Val Thr Pro Ser Val Pro Ala Gln
65 70 75 80

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Phe Leu Ser Lys Thr Leu Leu Arg Glu Arg Arg Ala Asp Asp Asp Tyr
85 90 95

Asn Lys Leu Val Pro Tyr Phe Val Leu Gly Asp Ile Trp Asp Ser Phe
100 105 110

Ala Glu Trp Ser Ala Tyr Gly Thr Gly Val Pro Leu Val Leu Asn Asn
115 120 125

Asn Lys Asp Arg Val Ile Gln Tyr Tyr Val Pro Ser Leu Ser Ala Ile
130 135 140

Gln Ile Tyr Ala His Ser His Ala Leu Asp Ser Ser Leu Lys Ser Arg
145 150 155 160

Arg Pro Gly Asp Ser Ser Asp Ser Asp Phe Arg Asp Ser Ser Ser Asp
165 170 175

Val Ser Ser Asp Ser Asp Ser Glu Arg Val Ser Ala Arg Val Asp Cys
180 185 190

Ile Ser Leu Arg Asp Gln His Gln Glu Asp Ser Ser Ser Asp Asp Gly
195 200 205

Glu Pro Leu Gly Ser Gln Gly Arg Leu Met Phe Glu Tyr Leu Glu Arg
210 215 220

Asp Leu Pro Tyr Ile Arg Glu Pro Phe Ala Asp Lys Val Leu Asp Leu
225 230 235 240

Ala Ala Gln Phe Pro Glu Leu Met Thr Leu Arg Ser Cys Asp Leu Leu
245 250 255

Arg Ser Ser Trp Phe Ser Val Ala Trp Tyr Pro Ile Tyr Arg Ile Pro
260 265 270

Thr Gly Pro Thr Leu Lys Asp Leu Asp Ala Cys Phe Leu Thr Tyr His
275 280 285

Ser Leu His Thr Ser Phe Gly Gly Glu Gly Ser Glu Gln Ser Met Ser
290 295 300

Leu Thr Gln Pro Arg Glu Ser Glu Lys Met Ser Leu Pro Val Phe Gly
305 310 315 320

Leu Ala Ser Tyr Lys Phe Arg Gly Ser Leu Trp Thr Pro Ile Gly Gly
325 330 335

Ser Glu His Gln Leu Val Asn Ser Leu Phe Gln Ala Ala Asp Lys Trp
340 345 350

Leu His Ser Cys His Val Ser His Pro Asp Phe Leu Phe Phe Cys Arg
355 360 365

Arg

<210> 105

<211> 64

<212> DNA

<213> Artificial sequence

<220>

<223> oligo-dT + T7 promoter

<400> 105
ggccagtgaa ttgtaatacg actcactata gggaggcggt tttttttttt tttttttttt 60

tttv 64